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XX OS Homo sapiens.
XX FH Key
XX FT Region
XX FT Location/Qualifiers
XX FT 29..35
XX FT /label= CDR1
XX FT /note= "complementarity determining region"
XX FT 50..65
XX FT /label= CDR2
XX FT /note= "complementarity determining region"
XX FT 98..112
XX FT /label= CDR3
XX FT /note= "complementarity determining region"
XX FT
XX PN FR2724182-A1.
XX PD 08-MAR-1996.
XX PF 02-SEP-1994; 94FR-0010566.
XX PR 02-SEP-1994; 94FR-0010566.
XX PA (INSP ) INST PASTEUR.
XX PA (PROT-) PROTEINE PERFORMANCE.
XX PI Chaabihi H, Edelman L, Kaczorek M, Margaritte C;
XX PI WPI; 1996-162018/17.
XX DR N-PSDB; AAT26870.
XX FT
XX FT Recombinant anti-rhesus D monoclonal antibody - expressed by
XX FT baculovirus-transformed insect cells and useful for preventing
XX FT haemolysis in new-born babies
XX PS Example 1; Page 32; 46pp; French.
XX CC The human monoclonal antibody D7C2, of isotype IGM, recognises a
XX CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
XX CC cells. The antibody agglutinates rhesus positive cells but not
XX CC rhesus negative cells and is useful diagnostically and also for
XX CC preventing haemolysis in new-born rhesus positive babies.
XX CC Recombinant IGM-D7C2 can be produced by insect cells which have
XX CC been transformed by a baculoviral vector comprising a D7C2
XX CC expression cassette. The present sequence is that of the variable
XX CC region of the IGM-D7C2 heavy chain.
XX SQ Sequence 123 AA;

Alignment Scores:
Pred. No.: 1.26e-47 Length: 123
Score: 578.00 Matches: 109
Percent Similarity: 90.24% Conservativeness: 2
Best Local Similarity: 88.62% Mismatches: 4
Query Match: 77.79% Indels: 8
DB: 17 Gaps: 1

US-08-728-463B-205 (1-403) x AAW03757 (1-123)
QY 58 CAGCTGACGCTACAGCAGTGGCGCGAGGACTGTGAAGCTTCGGAGACCTGTCCCTC 117
Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20
QY 118 ACCTGCGCTGTCTACTGTGGTCCCTTCAGTGGTTACTACTGGAGCTGGATCCGCGACCCC 177
Db 21 ThrCysThrValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
QY 178 CCAGGTAAAGGGCTGGAGTGATTTGGGGAATCAATCATAGTGGAAACACCACTACAAC 237
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTyrAsn 60
QY 238 CCGTCCCTCAGAGTCGAGTCACCATATCAGTCGACAGCTCCAGACCACTCTCCCTG 297
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80

QY 298 AAGCTGAGCTGTGTGACCGCGCGACACGGCTGTGTATTACTGTCCGAGAGTAATT--- 354
Db 81 LysLeuAenSerValThrAlaAlaAspThrAlaValTyr-Tyr-CysAlaArgAlaProGlu 100
QY 355 -----AATTGGTTCGACCCCTGGGGCGAGGAGACCCCTGGTCACC 393
Db 101 TyrLysTrpLysTyrHisGlyAspTrpPheAspProTrpGlyGlnGlyThrThrValThr 120
QY 394 GTCCTCTCA 402
Db 121 ValSerSer 123

RESULT 14
AAR41285
ID AAR41285 standard; Protein; 142 AA.
XX AC AAR41285;
XX DT 01-NOV-1993 (first entry)
XX DE F105 rearranged variable region heavy chain.
XX KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
XX KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
XX KW chain; epitope; immune deficiency.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT /label= sig_peptide
XX FT Protein
XX FT /label= mat_protein
XX FT
XX PN W09312232-A.
XX PD 24-JUN-1993.
XX PF 10-DEC-1992; 92WO-US10928.
XX PR 10-DEC-1991; 91US-0804652.
XX PA (DAND ) DANA FARMER CANCER INST INC.
XX PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
XX FT
XX FT WPI; 1993-214174/26.
XX FT N-PSDB; AAQ49154.
XX FT
XX FT DNA segments encoding monoclonal antibody - which binds to gp120
XX FT and neutralises HIV, for treating AIDS, and for diagnosing and
XX FT monitoring HIV infection
XX PS Claim 9-10; Page 77; 109pp; English.
XX CC mRNA from the known hybridoma F105 was converted to cDNA and this
XX CC subjected to PCR amplification using primers corresp. to appropriate
XX CC parts of the heavy or light chains and having restriction sites to
XX CC permit cloning. The extension prods. were isolated and sequenced.
XX CC The recombinant human monoclonal antibody (MAb) binds to a
XX CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
XX CC the binding of gp120 to the CD4 receptor, and neutralises a broad
XX CC range of HIV isolates. The MAb may be used to treat immune
XX CC deficiency, esp. at doses of 0.1-10 mg/kg.
XX SQ Sequence 142 AA;

Alignment Scores:
Pred. No.: 2.33e-46 Length: 142
Score: 565.00 Matches: 110
Percent Similarity: 85.92% Conservativeness: 12

```

CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX SQ Sequence 249 AA;

Alignment Scores:  
 Pred. No.: 1,37e-48 Length: 249  
 Score: 588.50 Matches: 112  
 Percent Similarity: 89.68% Conservative: 1  
 Best Local Similarity: 88.89% Mismatches: 2  
 Query Match: 79.21% Indels: 11  
 DB: 23 Gaps: 1

US-08-728-463B-205 (1-403) x AAB45310 (1-249)

QY 58 CAGGTGACGTACAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCTGTCCCTC 117  
 DB 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
 QY 118 ACCTGCGCTGTCTATGTGGTCTCTTCACTGGTTACTGAGCTGGATCCGCCAGCCC 177  
 DB 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40  
 QY 178 CCAGGTAAGGGCTGGAGTGGGAAATCAATCATATGTCGAGCACCACCACTACAAC 237  
 DB 41 ProGlyLysGlyLeuGluTrpIleGlyLulLleAsnHisSerGlySerThrAsnTyrAsn 60  
 QY 238 CCGTCCCTCAAGAGTCAGTCACATATCATGTCGACACGTCCTCAAGAACCACTGTTCTCCCTG 297  
 DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80  
 QY 298 AAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGA----- 348  
 DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyProArg 100  
 QY 349 -----GTAATTAATTTGTTTCGACCCCTGGCGGCGCAGGGAACC 384  
 DB 101 TyrTyrAspIleLeuThrGlyTyrArgTyrAsnTrpPheAspProTrpGlyArgGlyThr 120  
 QY 385 CTGCTCACGTCCTCTCA 402  
 DB 121 LeuValThrValSerSer 126

RESULT 12

AAB36206  
 ID AAB36206 standard; protein; 473 AA.  
 AC AAB36206;

XX 15-FEB-2001 (first entry)

XX Human immune system associated protein HISAP-4.

XX Human; immune system associated protein; HISAP-4; immune disorder;  
 KW infection; autoimmune disease; cancer.

XX Homo sapiens.

XX US6135941-A.

XX 24-OCT-2000.

XX 27-MAR-1998; 98US-0049672.

XX 27-MAR-1998; 98US-0049672.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Lal P, Corley NC, Guégler KJ, Baughn MR;  
 PI Hillman JL, Au-Young J;

XX WPI; 2001-030926/04.  
 DR N-PSDB; AAC66522.

XX

PT New human immune system associated proteins (HISAP) and polynucleotides  
 PT encoding the HISAP; useful for diagnosing, treating or preventing  
 PT immune or cell proliferative disorders or infections

XX Claim 1; Column 53-56; 54pp; English.

XX The present invention provides the coding and protein sequences for a  
 CC number of human immune system associated proteins (HISAPs). These can be  
 CC used in the diagnosis and treatment of various autoimmune disorders,  
 CC infections and cell proliferation diseases. The diseases include AIDS,  
 CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
 CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
 CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
 CC erythematosus, arteriosclerosis, cirrhosis and cancer.

SQ Sequence 473 AA;

Alignment Scores:  
 Pred. No.: 1,41e-47 Length: 473  
 Score: 578.50 Matches: 118  
 Percent Similarity: 86.01% Conservative: 5  
 Best Local Similarity: 82.52% Mismatches: 11  
 Query Match: 77.86% Indels: 9  
 DB: 22 Gaps: 3

US-08-728-463B-205 (1-403) x AAB36206 (1-473)

QY 1 ATGAACACCTGTGTTCTTCTCTCTGTGGCAGTCCAGATGGTCTGTCCAG 60  
 DB 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 61 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCTGTCCCTCACC 120  
 DB 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
 QY 121 TGGCGTGTCTATGTGGTCTCTTCAGT-----GTTTACTGAGCTGGATCCGCCAG 174  
 DB 41 CysAlaValSerGlyGlySerIleThrSerGlyGlyTyrTyrTrpSerTrpIleArgGln 60  
 QY 175 CCCCAGGTAAAGGGCTGGAGTGGGGAATCAATCATATGTCGAGCACCACCACTAC 234  
 DB 61 ProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrLeuTyr 80  
 QY 235 AACCCGTCCTCAAGAGTCAGTCACCATATCAGTCACACAGCTCCAGAACCACTCTCC 294  
 DB 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100  
 QY 295 CTGAAGCTGAGCTCTGTGACCGCGGACACGCTGTGTATTACTGTGGAGAGTAATT 354  
 DB 101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAspAsp 120  
 QY 355 -----AATTGG-----TTCACCCCTGGGGCGCAGGAAACCTGGTCTCACC 393  
 DB 121 ValGlyLeuArgGlyGlyAsnTyrGlyMetAspValTrpGlyGlnGlyThrLeuValThr 140  
 QY 394 GTCTCTCTCA 402  
 DB 141 ValSerSer 143

RESULT 13

AAW03757  
 ID AAW03757 standard; Protein; 123 AA.

XX AAW03757;

XX 29-OCT-1996 (first entry)

XX Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.

XX Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;  
 KW rhesus positive; rhesus negative; haemolysis; heavy chain;  
 KW variable region; insect host cell; baculovirus; recombinant production.







CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 193 AA;

Alignment Scores:  
 Pred. No.: 2,21e-49 Length: 193  
 Score: 596.50 Matches: 117  
 Percent Similarity: 84.62% Conservative: 4  
 Best Local Similarity: 81.82% Mismatches: 13  
 Query Match: 80.28% Indels: 9  
 DB: 23 Gaps: 1

US-08-728-463B-205 (1-403) x ABP43199 (1-193)

QY 1 ATGAACACCTGGTTCCTCTCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60  
 DB |||||  
 QY 6 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 25  
 DB |||||  
 QY 61 GTCAGCTACAGCAGTGGGCGCAGGACTGTTCAAGCCTTCGGAGACCTGTCCTCACC 120  
 DB |||||  
 QY 26 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 45  
 DB |||||  
 QY 121 TGGCGTGTCTATGGTGGGCTCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCA 180  
 DB |||||  
 QY 46 CysThrValSerGlyGlySerIleSerSerTyrrTrpSerTrpIleArgGlnProPro 65  
 DB |||||  
 QY 181 GPTAAGGGCTGGAGTGGATGGGGAATCAATCATAGTGGAGCACCACCTACACCCG 240  
 DB |||||  
 QY 66 GlyLeuGlyLeuGluTrpIleGlyLeuTyrrTrpSerGlySerThrAsnTyrrAsnPro 85  
 DB |||||  
 QY 241 TCCTCAAGAGTCGAGTACCATATCATCATCATCATCATCATCATCATCATCATCATCAT 300  
 DB |||||  
 QY 86 SerLeuLysSerArgValThrIleSerValAepThrSerLysAsnGlnPheSerLeuLys 105  
 DB |||||  
 QY 301 CTGAGCTCTGTACCCCGGACACGGCTGTGTATTACTGTCCGAGA----- 348  
 DB |||||  
 QY 106 LeuSerSerValThrAlaAlaAepThrAlaValTyrrCysAlaArgGlyProTyrrSer 125  
 DB |||||  
 QY 349 -----GTAATTAATTGGTTCCGACCCCTGGCCGAGGACCCCTGTCTCACC 393  
 DB |||||  
 QY 126 SerSerTrpTyrrProArgAlaGluTyrrPheGlnHisTrpGlyGlnGlyThrLeuValThr 145  
 DB |||||  
 QY 394 GTCTCTCA 402  
 DB |||||  
 QY 146 ValSerSer 148

RESULT 6

AAR93166  
 ID AAR93166 standard; Protein; 472 AA.

XX AAR93166;

XX 30-OCT-1996 (first entry)

DE Anti-rhesus D recombinant antibody D7C2 heavy chain.

XX Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;

KW rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;

KW variable region; insect host cell; baculovirus; recombinant production.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= signal\_peptide  
 FT /note= "mouse VH signal peptide sequence encoded by  
 FT synthetic linker"  
 FT Protein 20..472  
 FT /label= heavy\_chain  
 FT /note= "human gamma 1 chain constant region  
 FT and the variable region from anti-rhesus D  
 FT antibody D7C2"  
 XX

PN FR2724182-A1.

XX 08-MAR-1996.

XX 02-SEP-1994; 94PR-0010566.

XX 02-SEP-1994; 94PR-0010566.

XX (INSP ) INST PASTEUR.

XX (PROT-) PROTEINE PERFORMANCE.

XX Chaabihi H, Edelman L, Kaczorek M, Margaritte C;

XX WPI; 1996-162018/17.

XX N-PSDB; AAT26889.

XX Recombinant anti-rhesus D monoclonal antibody - expressed by  
 baculovirus-transformed insect cells and useful for preventing  
 haemolysis in new-born babies

XX Example 2; Page 35-37; 46pp; French.

XX The human monoclonal antibody D7C2, of isotype IgM, recognises a  
 30-32 kD polypeptide on the membrane of rhesus positive red blood  
 cells. The antibody agglutinates rhesus positive cells but not  
 rhesus negative cells and is useful diagnostically and also for  
 preventing haemolysis in new-born rhesus positive babies.

XX Recombinant IGM-D7C2 can be produced by insect cells which have  
 been transformed by a baculoviral vector comprising a D7C2  
 expression cassette. The present sequence is that of a recombinant  
 IGM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.

XX Sequence 472 AA;

Alignment Scores:

Pred. No.: 3,58e-49 Length: 472  
 Score: 595.00 Matches: 115  
 Percent Similarity: 86.67% Conservative: 2  
 Best Local Similarity: 85.19% Mismatches: 10  
 Query Match: 80.08% Indels: 8  
 DB: 17 Gaps: 1

US-08-728-463B-205 (1-403) x AAR93166 (1-472)

QY 22 CTCCTCTGTGGCAGCTCCAGATGGTCTGTCCAGGTGCAGTACAGCAGTGGGC 81

DB 8 LeuPheLeuValAlaAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnTrpGly 27

QY 82 GCAGGACTGTGAAGCCTTCGGAGACCTGTCTCCCTACCTGCCGTGTCTATGTTGGTCC 141

DB 28 AlaGlyLeuLeuLysProSerGluThrLeuSerLeuThrCysThrValTyrrGlySer 47

QY 142 TTCAGTGTGTACTACTGGAGTCCGCCAGCCCCCAGGTAAAGGCTGGAGTGGATT 201

DB 48 PheSerGlyTyrrTrpSerTrpIleArgGlnProGlyLysGlyLeuGluTrpIle 67

QY 202 GGGGAAATCAATCATAGTGAAGCACCACCACTACAACCCGCTCCCTCAAGAGTCCAGTCCACC 261

DB 68 GlyGluIleAsnHisSerGlySerThrAsnTyrrAsnProSerLeuLysSerArgValThr 87

QY 262 ATATCAGTCGACAGCTCCAGAACCACTTCTCCCTGAGCTGAGTCTGTGTACCGCGCG 321

AA66324 standard; Protein; 116 AA.  
AA66324;  
03-AUG-1995 (first entry)  
Human immunoglobulin variable heavy chain #30.  
XX Primer; PCR; amplifly; human; immunoglobulin; variable; heavy chain;  
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.  
XX Homo sapiens.  
XX  
XX W09426895-A.  
XX  
XX 24-NOV-1994.  
XX  
XX 10-MAY-1993; 93WO-JP00603.  
XX  
XX 10-MAY-1993; 93WO-JP00603.  
XX (NIBS ) JAPAN TOBACCO INC.  
XX  
XX Honjo T, Matsuda F;  
XX  
XX WPI; 1995-006791/01.  
XX N-PSDB; AAQ78972.  
XX  
XX DNA fragment comprising human immunoglobulin Vh genes - for the  
PT production of human immunoglobulin in mammalian hosts  
XX  
XX Claim 41; Page 74-75; 130pp; Japanese.  
XX  
XX Protein sequences (AA66295-51) are novel human immunoglobulin heavy  
CC chain sequences encoded by novel isolated genes. The genes  
CC (AAQ78935-79002) were isolated and cloned from a series of cosmid  
CC constructs: Y202; Y103; Y21; Y6Y24; 3-31; M84; M18 and M131, by PCR  
CC amplification using primers AAQ78917-38. The genes are subdivided into 5  
CC families of Vh genes. The fragments cover a region of 800 kb. The DNA  
CC fragments were isolated from high molecular weight DNA from human  
CC placenta. The DNA was partially digested with Taqi restriction enzyme.  
CC The fragments were separated by gel electrophoresis and 35-45 kb fractions  
CC were collected. The fragments were ligated with ClaI-digested cosmid  
CC vector pJB81. The ligation products were in vitro packed and infected  
CC into E.coli 490A. The fragments were then subcloned by colony  
CC hybridisation. The Vh genes and the DNA fragments encoding them are  
CC useful in producing human immunoglobulin in mammalian hosts.  
XX  
XX Sequence 116 AA;  
SQ  
Alignment Scores:  
Pred. No.: 6.99e-52 Length: 116  
Score: 622.00 Matches: 116  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.71% Indels: 0  
DB: 16 Gaps: 0  
US-08-728-463B-205 (1-403) x AAR66324 (1-116)  
QY 1 ATGAACACCTGGTCTTCCTCCTCCTCGTGGCAGCTCCAGATGGTCTGTCACG 60  
Db 1 MethyHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
QY 61 GTGCAGCTACAGAGTGGCGGAGGACTGTGAAGCTTCGGAGACCTGTCCTCAAC 120  
Db 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLeuPysProSerGlnTrpLeuSerLeuThr 40  
QY 121 TGCCTCTCTATGGTGGTCTTTCAGTGGTTACTTACTGGAGCTGGATCCGCCAGCCCCA 180  
Db 41 CysAlaValTrpGlyGlySerPheSerGlyTrpTrpSerTrpIleArgGlnProPro 60  
QY 181 GGTAAGGGGCTGGAGTGGATGGGGAATCAATCATAGTGAAGACCACTACACCCG 240

Db 61 GlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTrpAsnPro 80  
QY 241 TCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCAGAACCCAGTTCCTCCCTGAAG 300  
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100  
QY 301 CTGACTCTGTGACCCGCGGACACCGCTGTGTATTACTGTGCGGAGA 348  
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTrpTyrCysAlaArg 116  
RESULT 5  
ABP43199  
ID ABP43199 standard; Protein; 193 AA.  
XX  
XX AC ABP43199;  
XX  
XX 22-AUG-2002 (first entry)  
XX  
XX DE Human ovarian antigen HVVDH44, SEQ ID NO:4331.  
XX  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.  
XX  
XX Homo sapiens.  
XX  
XX W0200200677-A1.  
XX  
XX 03-JAN-2002.  
XX  
XX 07-JUN-2001; 2001WO-US18569.  
XX  
XX 07-JUN-2000; 2000US-209467P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
PI  
XX WPI: 2002-147878/19.  
XX N-PSDB; ABQ56276.  
XX  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases -  
XX  
XX Claim 11; SEQ ID No 4331; 2922pp; English.  
XX  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,

CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia,  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.  
 XX

SQ Sequence 537 AA;

Alignment Scores:  
 Pred. No.: 1.77e-54 Length: 537  
 Score: 650.00 Matches: 128  
 Percent Similarity: 88.36% Conservative: 1  
 Best Local Similarity: 87.67% Mismatches: 5  
 Query Match: 87.48% Indels: 12  
 DB: 21 Gaps: 2

US-08-728-463B-205 (1-403) x AAY96290 (1-537)

QY 1 ATGAACACCTGTGGTCTTCTCCCTCCCTGGTGGCAGCTCCAGATGGTCTGTCCAG 60  
 DB 8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 27  
 QY 61 GTCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCCTGTCCCTCACC 120  
 DB 28 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 47  
 QY 121 TGGCTGTCTATGGTGGTCTCTC-----AGTGGTTACTACTGGAGCTGG 165  
 DB 48 CysAlaValTyrGlyGlySerPheSerGlyTyrTyrLeuSerGlyTyrTrpSerTrp 67  
 QY 166 ATCCGCGAGCCCGCAGTGAAGGGCTGGAGTGATGGGGAATCAATCATATGGAAC 225  
 DB 68 IleArgGlnProGlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySer 87  
 QY 226 ACCAATACACCCGCTCCCTCAAGAGTCGAGTCAGTCACCATATCAGTCGACACGTCGAAGA 285  
 DB 88 ThrAsnTyrAsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsn 107  
 QY 286 CAGTCTCCCTGAGTGTAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGG 345  
 DB 108 GlnPheSerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAla 127  
 QY 346 AGAGTAATTAAT-----TGCTTCGACCCCTGGGGCCAGGGAAC 384  
 DB 128 ArgGlyArgSerAspSerSerGlySerProTyrGlyLeuAspTyrTrpGlyGlnGlyThr 147  
 QY 385 CTGGTCACCGTCTCCTCA 402  
 DB 148 LeuValThrValSerSer 153

RESULT 3

ID AAB26884 standard; Protein; 462 AA.

AC AAB26884;

DT 01-FEB-2001 (first entry)

DE Human immunoglobulin heavy chain amino acid sequence.  
 XX Monoclonal antibody; immunoglobulin heavy chain; human.  
 KW Homo sapiens.  
 OS

XX WO200058499-A1.

XX 05-OCT-2000.

PD

XX

PF 30-MAR-2000; 2000WO-JP02022.  
 XX  
 PR 30-MAR-1999; 99JP-0087929.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Kusunoki C, Fukushima A;  
 XX  
 DR WPI; 2000-611721/58.  
 DR N-PSDB; AAA09695.  
 XX

Transformation of a hybridoma with a gene encoding an immunoglobulin heavy chain polypeptide for enhanced production of monoclonal antibody

Example 2; Page 40-43; 48pp; Japanese.

CC This invention relates to a method for the production of a monoclonal  
 CC antibody. The antibody is produced by inserting a gene encoding an  
 CC immunoglobulin heavy chain polypeptide into cells which produce a  
 CC monoclonal antibody recognizing the immunoglobulin, and culturing the  
 CC transformant to express the antibody. The invention also includes  
 CC monoclonal antibody-expressing cells transformed by the method; and  
 CC transgenic non-human animals containing the cells and expressing a human  
 CC antibody. The method results in the enhanced expression of a monoclonal  
 CC antibody for diagnostic and therapeutic use. The present sequence  
 CC represents a human immunoglobulin heavy chain amino acid sequence, the  
 CC cDNA encoding the protein is used in an example of the method of the  
 CC invention.

SQ Sequence 462 AA;

Alignment Scores:  
 Pred. No.: 4.2e-54 Length: 462  
 Score: 646.00 Matches: 123  
 Percent Similarity: 93.38% Conservative: 4  
 Best Local Similarity: 90.44% Mismatches: 7  
 Query Match: 86.94% Indels: 2  
 DB: 21 Gaps: 1

US-08-728-463B-205 (1-403) x AAB26884 (1-462)

QY 1 ATGAACACCTGTGGTCTTCTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCCAG 60  
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 61 GTCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACC 120  
 DB 21 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 40  
 QY 121 TGGCTGTCTATGGTGGTCTCTCAGTGGTTACTTGGAGTGGATCGGACCGCCAGCCCA 180  
 DB 41 CysAlaValTyrGlyGlySerPheSerGlyTyrTrpTrpIleArgGlnProPro 60  
 QY 181 GGTAAAGGGCTGGAGTGGATGGGGAATCAATCATATAGTGAAGCACCACCAACCCG 240  
 DB 61 GlyLysGlyLeuGluTrpIleGlyGluIleIleHisGlyAsnThrAsnTyrAsnPro 80  
 QY 241 TCCCTCAGAGTCGAGTCACCATATCAGTCGACAGCTCCAGAACACAGTTCCTCCCTGAAG 300  
 DB 81 SerLeuLysSerArgValSerIleSerValAspThrSerLysAsnGlnPheSerLeuThr 100  
 QY 301 CTGAGCTCTGTGACCGCGGACACGGCTGTGTATTACTGTGGGAGA-----GTAAAT 354  
 DB 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyGlyAlaVal 120  
 QY 355 AATTGGTTCCACCCCTGGGCGCAGGGAACCCCTGGTCACCGCTCCTCA 402  
 DB 121 AlaAlaPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 136

RESULT 4  
 AAB66324





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 26.0666 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-205  
Perfect score: 743  
Sequence: 1 ATGAACACCTGGTGTCTTT.....CTGTGTCACCGTCTCTCTCAG 403

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 101002.\*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	680.5	91.6	139	21	AA999556	Human LH11238 mono
2	650	87.5	537	21	AA996290	Human IGFAM-2 immu
3	646	86.9	462	21	AA268884	Human immunoglobul
4	622	83.7	116	16	AA66324	Human immunoglobul
5	596.5	80.3	193	23	ABP43199	Human ovarian anti
6	595	80.1	472	17	AA993166	Anti-thesus D reco
7	592.5	79.7	133	23	ABG35331	Thrombopoietin ago
8	592.5	79.7	256	23	ABG35335	Thrombopoietin ago
9	592.5	79.7	266	23	ABG35336	Thrombopoietin ago
10	590.5	79.5	139	21	AA82628	Human PTHP monocl
11	588.5	79.2	249	23	ABP45310	Human Blys binding
12	578.5	77.9	473	22	AA36206	Human immune syate
13	578	77.8	123	17	AAW03757	Anti-thesus D mono
14	565	76.0	142	14	AA41285	F105 rearranged va
15	564.5	76.0	139	21	AA964676	Human 5' EST relat
16	560.5	75.4	244	20	AA21883	Amino acid sequenc
17	558	75.1	241	22	AA46061	Human TP anti-idio
18	555.5	74.8	249	23	ABP44946	Human Blys binding
19	554.5	74.6	132	22	AA62247	Human gene 4-encod
20	554.5	74.6	141	22	AA62249	Human gene 4-encod
21	551	74.2	136	18	AAW24536	Immunoglobulin rB6
22	551	74.2	476	18	AAW01822	Primate anti-hu
23	551	74.2	476	19	AAW63765	Macaque primatized
24	551	74.2	476	23	AAU11646	Protein sequence o
25	550.5	74.1	139	21	AA956713	Amino acid sequenc
26	550	74.0	116	14	AA42689	Vh 71-4. Homo sap
27	550	74.0	116	16	AA66346	Human immunoglobul
28	548.5	73.8	487	22	AA90607	Human secreted pro
29	548.5	73.8	487	23	ABG5445	Human albumin fusi
30	543	73.1	255	23	ABP45631	Human Blys binding
31	541	72.8	470	21	AA44721	Human immune syste
32	540.5	72.7	128	12	AA412269	Anti-human Rhd FOM
33	540	72.6	253	23	ABP45322	Human Blys binding
34	539.5	72.6	254	23	ABP45648	Human Blys binding
35	539.5	72.6	507	21	AA96304	Human IGFAM-16 imm
36	539	72.5	118	16	AA66348	Human immunoglobul
37	538	72.4	116	16	AA66298	Human immunoglobul
38	536	72.1	121	12	AA412270	Anti-human Rhd FOM
39	535.5	72.1	141	21	AA956728	Amino acid sequenc
40	535.5	72.1	250	22	ABP45402	Human Blys binding
41	535	72.0	120	23	ABG2758	Human HIV-1 monocl
42	534	71.9	140	18	AAW32477	Anti-CD4 cymomolgu
43	534	71.9	140	19	AAW43430	Monkey anti-CD4 he
44	534	71.9	141	14	AA31948	Anti-CD4 VH peptid
45	534	71.9	467	18	AAW14927	Human gamma-4PE he

ALIGNMENTS

RESULT 1  
AA999556  
ID AA999556 standard; Protein; 139 AA.  
XX  
AC AA999556;  
XX  
DT 20-SEP-2000 (first entry)  
XX  
DE Human LH11238 monoclonal antibody heavy chain variable region.  
XX  
KW Human: LH11238 monoclonal antibody; hybridoma; tumour-specific; cancer;  
KW cytotoxic; cytotoxic; heavy chain variable region.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..139

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.64416 Seconds  
(without alignments)  
4373.264 Million cell updates/sec

Title: US-08-728-463B-205  
Perfect score: 743  
Sequence: 1 ATGAACACCTGTGTTCTT.....CTGGTCACCGTCTCTCTAG 403

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q/cgn2 1/USPTO spool/US08728463/runat\_03062003 085614 16804/app query.fasta\_1.3690  
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	579	77.9	146	1 HV21 HUMAN	P06331 homo sapien
2	402	54.1	129	1 HV2F HUMAN	P01824 homo sapien
3	396	53.3	117	1 HV2G HUMAN	P01825 homo sapien
4	393.5	53.0	137	1 HV46 MOUSE	P01822 mus musculus
5	370	49.8	116	1 HV60 MOUSE	P18531 mus musculus
6	358	48.2	144	1 HV43 MOUSE	P01819 mus musculus
7	354	47.6	113	1 HV47 MOUSE	P01823 mus musculus
8	343	46.2	116	1 HV61 MOUSE	P18532 mus musculus
9	336	45.2	135	1 HV02 XENLA	P20957 xenopus lae
10	326.5	43.9	117	1 HV62 MOUSE	P01808 mus musculus
11	326.5	43.9	119	1 HV38 MOUSE	P03980 mus musculus
12	326	43.9	138	1 HV48 MOUSE	P01751 mus musculus
13	322.5	43.4	139	1 HV07 MOUSE	P01811 mus musculus
14	321	43.2	117	1 HV41 MOUSE	P04438 homo sapien
15	318.5	42.9	147	1 HV2H HUMAN	P01807 mus musculus
16	317.5	42.7	119	1 HV37 MOUSE	P01820 mus musculus
17	316	42.5	115	1 HV44 MOUSE	P01810 mus musculus
18	314.5	42.3	119	1 HV40 MOUSE	

19	311.5	41.9	136	1 HV01 XENLA	P20956 xenopus lae
20	311	41.9	142	1 HV01 RAT	P01805 rattus norv
21	308.5	41.5	137	1 HV11 MOUSE	P01755 mus musculus
22	308	41.5	118	1 HV39 MOUSE	P01809 mus musculus
23	305	41.0	117	1 HV12 MOUSE	P01756 mus musculus
24	304	40.9	116	1 HV45 MOUSE	P01821 mus musculus
25	303.5	40.8	120	1 HV50 MOUSE	P06329 mus musculus
26	300	40.4	117	1 HV13 MOUSE	P01757 mus musculus
27	298.5	40.2	114	1 HV3B HUMAN	P01763 homo sapien
28	296.5	39.9	122	1 HV3G HUMAN	P01768 homo sapien
29	294	39.6	121	1 HV01 MOUSE	P01745 mus musculus
30	293.5	39.5	118	1 HV51 MOUSE	P06330 mus musculus
31	290.5	39.1	117	1 HV04 MOUSE	P01748 mus musculus
32	288.5	38.8	120	1 HV2B HUMAN	P01815 homo sapien
33	288.5	38.8	122	1 HV3A HUMAN	P01762 homo sapien
34	288	38.8	117	1 HV42 MOUSE	P01812 mus musculus
35	288	38.8	123	1 HV25 MOUSE	P01794 mus musculus
36	287.5	38.7	116	1 HV36 MOUSE	P01806 mus musculus
37	287	38.6	115	1 HV3D HUMAN	P01765 homo sapien
38	287	38.6	116	1 HV05 CARAU	P19181 carassius a
39	287	38.6	140	1 HV02 MOUSE	P01746 mus musculus
40	286	38.5	119	1 HV3I HUMAN	P01770 homo sapien
41	285	38.4	121	1 HV3J HUMAN	P01771 homo sapien
42	284	38.2	117	1 HV17 MOUSE	P01786 mus musculus
43	282.5	38.0	122	1 HV20 MOUSE	P01789 mus musculus
44	281.5	37.9	117	1 HV09 MOUSE	P01753 mus musculus
45	281.5	37.9	117	1 HV3C HUMAN	P01764 homo sapien

#### ALIGNMENTS

RESULT 1  
HV21 HUMAN  
ID HV21 HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85205332; PubMed=3922855;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT 'A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.';  
RL Gene 33:181-189(1985).  
DR PIR; A02101; GIHUH2.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
FT DOMAIN 20 117 V SEGMENT.  
FT DOMAIN 118 127 D SEGMENT.  
FT DOMAIN 128 146 J SEGMENT.  
FT DISULFID 42 115 BY SIMILARITY.  
FT NON\_TER 146 146  
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD528B218171F CRC64;  
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Score: 579.00 Matches: 118  
Percent Similarity: 83.67% Conservative: 5  
Best Local Similarity: 80.27% Mismatches: 11  
Query Match: 77.93% Indels: 14  
DB: 1 Gaps: 3

US-08-728-463B-205 (1-403) x HV2I\_HUMAN (1-146)

QY 1 ATGAACACCTGTGGTCTTCTCCCTCTGCTGGAGCTCCAGATGG-----GTCTGTC 56  
 Db 1 MetLysHisLeuTrpPheLeuLeuLeu-Leu-TyrCysGlnLeuProAspValGlyValLeuSe 20  
 QY 57 CAGGTGACAGTACACAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCT 116  
 Db 20 rGlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuValLysProSerGluThrLeuSerLe 40  
 QY 117 CACTCCGCTGCTATGTTGGTCTCTCAGTGGTACTACTGAGCTGATCCGACCC 176  
 Db 40 uThrCysAlaValPheGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPr 60  
 QY 177 CCAGTAAGGGCTGGAGTGGGGAATCAATCATAGTGAAGCACCACCACTCAA 236  
 Db 60 oProGlyArgGlyLeuGluTrpIleGlyGluLeuHisSerGlySerThrAsnTyrFly 80  
 QY 237 CCGTCCCTCAAGAGTCAGTCCATATCAGTCGACAGCTCCAGAACCACTTCTCCCT 296  
 Db 80 sThrSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnLeuPheSerLe 100  
 QY 297 GAAGTGTAGCTGTGTACCGCGGACACGCTGTGTATTACTGTGGCAGATAAT-- 354  
 Db 100 uLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyLeuLe 120  
 QY 355 -----AATGG-----TTGACCCCTGGGGCCAGGGAAC 383  
 Db 120 uArgGlyGlyTrpAsnAspValAspTyrTyrGlyMetAspValTrpGlyGlnGlyTh 140  
 QY 384 CTGTGTACCGTCTCTCTCA 402  
 Db 140 rThrValThrValSerSer 146

RESULT 2  
 HV2F HUMAN  
 ID HV2F HUMAN STANDARD; PRT; 129 AA.  
 AC P01824;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region WAH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8222235; PubMed=6806818;  
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;  
 RT "Complete amino acid sequence of the delta heavy chain of human  
 immunoglobulin D.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA  
 CC PROTEIN.  
 DR PIR; A02099; D2HUMA.  
 DR HSP; P01825; 7FAB.  
 DR GlycoSuiteDB; P01824; --  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.  
 DR Immunoglobulin V region.  
 KW NON\_TER 129  
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Alignment Scores:  
 Pred. No.: 1.45e-30 Length: 129  
 Score: 402.00 Matches: 80  
 Percent Similarity: 72.87% Conservative: 14  
 Best Local Similarity: 62.02% Mismatches: 21  
 Query Match: 54.10% Indels: 14

US-08-728-463B-205 (1-403) x HV2F\_HUMAN (1-129)

QY 58 CAGTGCAGCTACAGAGTGGGGCGCAGGACTGTTGAAGCCTTCGAGACCTGTCTCCCTC 117  
 Db 1 ArgLeuGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20  
 QY 118 ACTGCGCTCTCATGTGGTCTCTTC-----AGTGGTTACTACTGGAGCTGGATCCGC 171  
 Db 21 ThrCysIleValSerGlyGlyProIleArgArgThrGlyTyrTyrTrpGlyTrpIleArg 40  
 QY 172 CAGCCCCAGGTAAAGGGCTGGAGTGGGAAATCAATCATAGTGAAGCACCACCAAC 231  
 Db 41 GlnProGlyLysGlyLeuGluTrpIleGlyValTyrTyrThrGlySerIleTyr 60  
 QY 232 TACAACCCCTCCCTCAAGAGTCCAGTCCATATCAGTCGACAGCTCCAGAACCACTTCT 291  
 Db 61 TyrAsnProSerLeuArgGlyArgValThrIleSerValAspThrSerArgAsnGlnPhe 80  
 QY 292 TCCTCAAGCTGAGCTCTGTGACCGCGGACACGGCTGTGTATTACTGTGCGAGA--- 348  
 Db 81 SerLeuAsnLeuArgSerMetSerAlaAlaAspThrAlaMetTyrTyrCysAlaArgGly 100  
 QY 349 -----GTAATTAATGTTGTTGACCCCTGGGC 375  
 Db 101 AsnProProTyrTyrAspIleGlyThrGlySerAspAspGlyIleAspValTrpGly 120  
 QY 376 CAGGGAACCTGTGACCGTCTCTCTCA 402  
 Db 121 GlnGlyThrThrValHisValSerSer 129

RESULT 3  
 HV2G HUMAN  
 ID HV2G HUMAN STANDARD; PRT; 117 AA.  
 AC P01825;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region NEMW.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77242302; PubMed=407927;  
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;  
 RT "Amino acid sequence of the VH region of a human myeloma  
 immunoglobulin (IGG New).";  
 RL Biochemistry 16:3412-3420(1977).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 DR PIR; A02100; GIHUM.  
 DR PDB; 7FAB; 31-JAN-94.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.  
 DR Immunoglobulin V region; 3D-structure.  
 KW MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT TURN 30 31

```
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Alignment Scores:
Pred. No.: 5 33e-30 Length: 117
Score: 396.00 Matches: 76
Percent Similarity: 81.20% Conservative: 19
Best Local Similarity: 64.96% Mismatches: 20
Query Match: 53.30% Indels: 2
DB: 1 Gaps: 1

US-08-728-463b-205 (1-403) x HV2G_HUMAN (1-117)

QY 58 CAGGTGACGCTACGACGAGTGGCGGCGAGGACTGTTGAAGCTTCGGAGACCCCTGTCCCTC 117
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeu 20
QY 118 ACTGCGCTGCTATGTTGGTGGTCCCTCAGTGGTTACTCTGAGAGTGGATCCGCCAGCCC 177
Db 21 ThrCysThrValSerGlySerThrPheSerAsnAspTyrThrTrpValArgGlnPro 40
QY 178 CCAGGTAAGGCTGAGTGGATGGGAATCAATCATAGTAGTGAAGCACCACCACTACAAC 237
Db 41 ProGlyArgGlyLeuGlnTrpIleGlyTyrValPheTyrHisGlyThrSerAspThr 60
QY 238 CCCTCCCTCAAGAGTCCAGTCCACATATCATGTCGACACGTCGACCAAGACCACTGTTCTCCCTG 297
Db 61 ThrProLeuArgSerArgValThrMetLeuValAspThrSerLysGlnPheSerLeu 80
QY 298 AAGCTGAGTCTGTGACCGCGCGGACACGGCTGTGTATTAATCTGTCGAGA-----GTA 351
Db 81 ArgLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgAsnLeuIle 100
QY 352 ATTAATTTGTTCCACCCCTGGCGCCAGGACCCCTGTCACCGCTCCCTCA 402
Db 101 AlaGlyCysIleAspValTrpGlyGlnGlySerLeuValThrValSerSer 117

RESULT 4
HV46 MOUSE STANDARD; PRT; 137 AA.
ID HV46 MOUSE
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
```

```
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RT immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
RT chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC -----
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CC -----
CC EMBL; M27638; AAA61337.1; -
DR EMBL; X07880; CAA30727.1; -
DR PIR; P01825; 7FAB.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 77 78 GV -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Alignment Scores:
Pred. No.: 9 36e-30 Length: 137
Score: 393.50 Matches: 82
Percent Similarity: 73.19% Conservative: 19
Best Local Similarity: 59.42% Mismatches: 32
Query Match: 52.96% Indels: 5
DB: 1 Gaps: 3

US-08-728-463b-205 (1-403) x HV46_MOUSE (1-137)

QY 1 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
```

```

Db      1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro---GlyIleMetSerAsp 19
        ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY      61 GTGAGCTACAGCAGTGGGGCGGAGCTGTGTGAGCCCTTCGGAGACCCCTCTCCCTCACC 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      20 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerLeuSerLeuThr 39
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121 TGCCTGTCTATGTGGTCTCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      40 CysSerValThrGlyTyrSerIleThrSerGlyTyrPheTyrPheTyrIleArgGlnPhe 59
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      178 CCAGTAAGGGCTGGAGTGGATTCGGGAATCAATCATAGTGAAGCACCACCACTACAAC 237
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      60 ProGlyAsnLysLeuGlnLysLeuGlnLysLeuGlnLysLeuGlnLysLeuGlnPheLeu 79
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      238 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTGCCAAGAACCGATCTCCCTG 297
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      80 ProSerLeuLysAsnArgValSerIleThrArgAspThrSerGluAsnGlnPhePheLeu 99
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      298 AAGCTGAGCTCTGTACCCCGCGGACACGCTGTGTATTACTGTGCG-----AGA 348
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      100 LysLeuAsnSerValThrGluAspThrAlaThrTyrCysAlaGlyAspAsnAsp 119
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      349 GTAATTATTGGTTCGACCCCTGGGCGGAGGAGCCCTGGTCACCGCTCTCTCA 402
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      120 HisLeuTyrTyrPheAspTyrTrpGlyGlnGlyThrThrThrValSerSer 137
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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## RESULT 5

```

HV60 MOUSE
ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR; JT0509; HVMS31.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03B53DC9E10 CRC64;

```

## Alignment Scores:

```

Pred. No.: 1.58e-27 Length: 116
Score: 370.00 Matches: 75
Percent Similarity: 76.92% Conservative: 15
Best Local Similarity: 64.10% Mismatches: 25
Query Match: 49.80% Indels: 2
DB: 1 Gaps: 2

```

```

US-08-728-463B-205 (1-403) x HV60_MOUSE (1-116).
QY      1 ATGAACACACTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro---GlyIleLeuSerAsp 19
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61 GTGAGCTACAGCAGTGGGGCGGAGCTGTGTGAGCCCTTCGGAGACCCCTCTCCCTCACC 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      20 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerLeuSerLeuThr 39
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121 TGCCTGTCTATGTGGTCTCTTC---AGTGGTTACTACTGGAGCTGGATCCGCCAGCCC 177
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      40 CysSerValThrGlyTyrSerIleThrSerGlyTyrTyrTyrPheTyrPheTyrIleArgGlnPhe 59
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      178 CCAGTAAGGGCTGGAGTGGATTCGGGAATCAATCATAGTGAAGCACCACCACTACAAC 237
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      60 ProGlyAsnLysLeuGlnLysLeuGlnLysLeuGlnLysLeuGlnLysLeuGlnPheLeu 79
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      238 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTGCCAAGAACCGATCTCTCCCTG 297
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      80 ProSerLeuLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPhePheLeu 99
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      298 AAGCTGAGCTCTGTACCCCGCGGACACGCTGTGTATTACTGTGCGCGAGA 348
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      100 LysLeuAsnSerValThrGluAspThrAlaThrTyrTyrCysAlaArg 116
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

## RESULT 6

```

HV43 MOUSE
ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RL of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -! MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC
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CC
CC EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MSG14.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

```

## Alignment Scores:

```

Pred. No.: 2.23e-26 Length: 144
Score: 358.00 Matches: 74
Percent Similarity: 66.67% Conservative: 22

```







```

Percent Similarity: 69.49%      Conservative: 17
Best Local Similarity: 55.08%    Mismatches: 33
Query Match: 43.94%             Indels: 3
DB: 1                            Gaps: 2

US-08-728-463B-205 (1-403) x HV38_MOUSE (1-119)

Qy 58 CAGGTGCAGCTACAGCAGCTGGGGGGGAGCAGTGTGAAGCCCTTCGGAGACCCCTGTCCCTC 117
Db 1 GluValLysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuLysLeu 20
Qy 118 ACCTGGCGTGTCTATGTGTGGGTCTTCAAGTGTACTACTGAGCTGGATCCGCCAGCCCC 177
Db 21 SerCysAlaAlaSerGlyPheAspPheSerArgTyrTrpMetSerTrpValArgGlnAla 40
Qy 178 CCAGGTAAGGGCGTGGAGTGGATGGGGAAATCAATCATAGTGGGAAGCACC---RAC 234
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluLeuAsnProAspSerSerThrIleAsnTyr 60
Qy 235 AACCCGTCCTCAAGAGTCGAGTCACCATATCAGTCGACACGCTCAAGAACACAGTTCTCC 294
Db 61 ThrProSerLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyr 80
Qy 295 CTGAAGCTGAGCTCTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTA--- 351
Db 81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrTy-CysAlaArgLeuGly 100
Qy 352 ---ATTAATGGTTCGACCCCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 402
Db 101 TyrTyrGlyTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer 118

RESULT 12
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Last created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Alignment Scores:
Pred. No. 2.44e-23 Length: 138

```

```
Score: 326.00 Matches: 66
Percent Similarity: 67.16% Conservative: 24
Best Local Similarity: 49.25% Mismatches: 40
Query Match: 43.88% Indels: 4
DB: 1 Gaps: 2

US-08-728-463B-205 (1-403) x HV48_MOUSE (1-138)

QY 13 TGGTTCCTTCCTCTGTCGGAGCTCCAGATGGGTCTGTCCTCCAGGTGCAGCTACAG 72
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 5 TyrilelleLeuPheLeuValAlaThrAlaThrAspValHisSerGlnValGlnLeuGln 24
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 73 CAGTGGGGCGGAGACTGTTGAAGCTTCGGAGACCTGTCCTCCACTCGGCTGTCTAT 132
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 25 GlnProGlyAlaGluLeuValProGlyAlaSerValGlnLeuSerCysLeuAlaSer 44
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 133 GGTGGGTCCTTCAGTGGTACTCTGGAGCTGGATCCGACGCCCGCCAGGTGAAGGGCTG 192
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 45 GlyHisThrPheThrAsnTyrTrpIleHisTrpVallysGlnArgProGlyGlnGlyLeu 64
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 193 GAGTGGATGGGGAATCAAT---CATAGTGAAGACCAACTACAAACCGTCCCTCAAG 249
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 65 GluTrpIleGlyGluIleAsnProAsnAspGlyArgSerAsnTyrAsnGluLysPheLys 84
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 250 AGTCGAGTCACCATATCAGTCGACACCTCCAGAACCCAGTCTCTCCCTGAAGCTGAGTCT 309
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 85 AsnIysAlaThrLeuThrValAspLysSerSerThrAlaTyrMetGlnLeuSerSer 104
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 310 GTGACCCCGCGGACACGGCTGTGTATTAATCTGTCGAGA-----GTAATTAATGG 360
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 105 LeuThrProGluGluPheAlaValTyrTyrCysAlaArgSerAspGlyTyrTyrAspTrp 124
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 361 TTCACCCCTGGGGCGGACCGCTGTCACCGTCTCTCTCA 402
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 125 PheValTyrTrpGlyGlnGlyThrLeuValThrPheSerAla 138

RESULT 13
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC ENBL; J00529; AAA38170.1; --
CC PIR; A02034; MHMS18.
CC HSSP; P01810; 2FBJ.
DR InterPrb; IPR003006; Ig_MHC.
```

```
RT immunoglobulin VH sequences";
RL Ann. Immunol. (Paris) 132D:77-88(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
CC PROTEIN BINDING 2.6-LEVAN.
CC -----
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CC -----
DR EMBL; M36631; AAA38078.1; --
DR PIR; A02081; G2MSUL.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117
FT SEQUENCE 117 AA; 13001 MW; B20A1074F8B99E7F CRC64;
SQ
Alignment Scores:
Pred. No.: 7.18e-23 Length: 117
Score: 321.00 Matches: 65
Percent Similarity: 68.91% Conservatives: 17
Best Local Similarity: 54.62% Mismatches: 31
Query Match: 43.20% Indels: 6
DB: 1 Gaps: 3
US-08-728-463B-205 (1-403) x HV41_MOUSE (1-117)
QY 58 CAGGTGAGTACAGAGTGGCGGAGGAGTCTTGAAGCTTCGGAGACCTGTCCCTC 117
DB 1 GluValLysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlySerLeuLysLeu 20
QY 118 ACTGCGCTGTCTATGGTGGGTCCTTCAGTGGTACTACTGGAGTGGATCCGCCAGCCC 177
DB 21 SerCysAlaAlaSerGlyPheAspPheSerGlyTyr-TripMetSerTrpValArgGlnAla 40
QY 178 CAGGTAAGGGCTGAGTGGATTTGGGAATCAATCAGTAGTGAGACCC---AACTAC 234
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnProAspSerThrIleAsnTyr 60
QY 235 AACCCGTCTCCTCAAGAGTCCAGTCCACATATCAGTCGACGCTCCAAAGAACCCAGTTCTCC 294
DB 61 ThrProPheLeuLysAspLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuPhe 80
QY 295 CTGAAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGAGTAATT 354
DB 81 LeuGlnMetSerLysValArgSerGluAspThrAlaLeuTyrPheCysAlaArg----- 98
QY 355 AATTGG-----TTGACCCCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTCA 402
DB 99 AsnTrpAspValGlyPheAspTyrTrpGlyGlnValThrThrLeuThrValSerSer 117
RESULT 15
ID HV2H_HUMAN STANDARD; PRT; 147 AA.
AC P04438;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region SESS precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RX MEDLINE=84298107; PubMed=6089186;
```

```
RA Takahashi N., Noma T., Honjo T.;
RT "Rearranged immunoglobulin heavy chain variable region (VH)
RT pseudogene that deletes the second complementarity-determining
RT region.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
DR PIR; A02090; G2HUUS.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SESS.
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147
FT SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB6666 CRC64;
SQ
Alignment Scores:
Pred. No.: 1.27e-22 Length: 147
Score: 318.50 Matches: 71
Percent Similarity: 62.41% Conservatives: 17
Best Local Similarity: 50.35% Mismatches: 39
Query Match: 42.87% Indels: 14
DB: 1 Gaps: 2
US-08-728-463B-205 (1-403) x HV2H_HUMAN (1-147)
QY 22 CTCCTCTGGTGGCAGCTCCAGATGGGTCCTGTCTCCAGTGCAGTACAGCAGTGGGC 81
DB 8 LeuLeuLeuLeuThrValProSerGlyValLeuSerGlnValAsnLeuArgGluSerGly 27
QY 82 CGAGGACTCTTCAAGCCTTCGGAGACCTGTCCCTCACCTGCGCTGTCTATGTGGTCC 141
DB 28 ProAlaLeuValLysAlaThrHisThrLeuThrLeuThrCysThrPheSerGlyLeuSer 47
QY 142 TTCAGT-----GGTTACTACTGGAGTGGATCCGCGACGCTGGATTAAGGGCTGGAG 195
DB 48 ValAsnThrArgGlyMetSerValSerTrpIleArgGlnProProGlyLysAlaLeuGlu 67
QY 196 TGGATTGGGGAATCAATCATATAGTGGAGCACCACCACTACACCGCTCCCTCAGAGTCGA 255
DB 68 TrpLeuAlaArgIleAspTrpAspAspLysTyrTyrGlyThrSerLeuGluThrArg 87
QY 256 GTCACCATATCAGTCGACACGCTCCAGAACCAAGTTCCTCCCTGAAGCTGAGCTGTGACC 315
DB 88 LeuThrIleSerLysAspThrSerLysAsnGlnValValLeuLysValThrAsnMetAsp 107
QY 316 GCGCGGACACGGCTGTGTATTACTGTGCGAGAGTA----- 351
DB 108 ProAlaAspThrAlaThrTyrTyrCysAlaArgMetGlnValThrMetValArgGluVal 127
QY 352 -----ATTAATTGGTTCCAGCCCTCGGCGCCAGGGAACCTGTGTACCGTCTCCTCA 402
DB 128 MetIleThrSerAsnAlaPheAspIleTrpGlyGlnGlyThr-TripSerProSerLeuGly 147
QY 403 G 403
DB 147 n 147
Search completed: June 3, 2003, 09:04:01
Job time : 9.64416 secs
```

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```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Alignment Scores:
Pred. No.: 1,82e-27 Length: 613
Score: 353.50 Matches: 71
Percent Similarity: 67.15% Conservative: 21
Best Local Similarity: 51.82% Mismatches: 42
Query Match: 47.58% Indels: 3
DB: 11 Gaps: 2

US-08-728-463B-205 (1-403) x Q8VCX7 (1-613)
Qy 1 ATGAACACCTGCTGTTCTTCCTCCTCGTGGCAGCTCCAGATGGTGCTCTGTCACG 60
Db 1 MetGluTrpThrTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisSerGln 20
Qy 61 GTCACGCTACAGAGTGGGGCCAGGACTGTGAAGCTTCGAGAGACCCTGTCCCTCAC 120
Db 21 ValGlnLeuGlnSerGlyAlaGluLeuMetLysProGlyAlaSerValLysIleSer 40
Qy 121 TGGCGTGTCTAGTGGTGGCTTCAGTGGTACTACTGGAGCTGGATCCGCCGCCCA 180
Db 41 CysLysAlaThrGlyTyrThrPheSerSerTyrTrpLeuGluTrpValLysGlnArgPro 60
Qy 181 GGTAAAGGGCTGGAGTGGATTGGGAAATC---AATCATAGTGAAGCACCACTACAAC 237
Db 61 GlyHisGlyLeuGluTrpLeuGlyGluLeuLeuProGlySerGlySerThrAsnTyrAsn 80
Qy 238 CGGTCCCTCAAGAGTCGAGTCACCATATFCAGTCGCACACGCTCCAGAACCAAGTTCTCCCTG 297
Db 81 GluLysPheLysGlyLysAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMet 100
Qy 298 AAGCTGAGCTCTGTGACCGCCGACACGCTGTATTACTGTGGAGAGTAATTAAT 357
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgArgLeuGly 120
Qy 358 -----TGTTTCGACCTCGGGCCAGGAACCTGTGTCACCGTCTCCTCA 402
Db 121 ArgTyrTyrPheAspValTrpGlyAlaGlyThrValThrValSerSer 137

RESULT 14
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CN 8 scFv.
GN CN 8.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

Alignment Scores:
Pred. No.:      2,37e-35      Length:      479
Score:          430.50       Matches:     88
Percent Similarity: 76.47%    Conservative: 16
Best Local Similarity: 64.71% Mismatches:   29
Query Match:     57.94%      Indels:      3
DB:              11         Gaps:       3

US-08-728-463B-205 (1-403) x Q99M22 (1-479)

Qy  1  ATGAAACACTGTGGTTCTCCTCTGTGGCGAGCTCCAGATGGTGCTGTGCCAG 60
Db  1  MetLysValLeuSerLeuLeuTyrLeuLeuThrAlaIlePro---GlyIleLeuSerAep 19

Qy  61  GTGCAGCTACAGCAGTCAGTGGGGCGCAGCACTGTGAAGCCCTCGGAGACCCTGTCCCTCAC 120
Db  20  ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnSerLeuSerLeuThr 39

Qy  121 TGGCGTCTCATGTGGTGGTCCCTC---AGTGGTTACTACTGGAGCTGATCCGCCAGCCC 177
Db  40  CysSerValThrGlyTyrSerIleThrSerGlyTyrTyrTrpAsnTrpIleArgGlnPhe 59

Qy  178 CCAGGTAAAGGGCTGAGTGGATTCCGGGAATCAATCATAGTGAAGCACCAACTACAAC 237
Db  60  ProGlyAsnLysLeuLeuTrpMetGlyTyrlleAsnTyrAspGlySerAsnAsnTyrAsn 79

Qy  238 CCCTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCAAGAAGACCAGTTCCTCCCTG 297
Db  80  ProSerLeuLysAsnArgileSerIleThrArgAspThrSerLysAsnGlnPhePheLeu 99

Qy  298 AAGCTGAGCTCTGTGACCCGCCCGGACACGGCTGTGTATTACTGTGCG---AGAGTAATT 354
Db  99  ::::

```

Db 100 LysLeuAanSerValThrThrGluAspThrAlaThrTyTyrCysAlaSerArgGlyTyr 117

Qy 355 AATTGGTTTCGACCCCTGGGGCCAGGAACCTGGTCACCGTCCTCTCA 402  
:::|||||  
Db 120 SerTrpPheProAsnTrpGlyGlnGlyThrLeuValThrValSerAla 135

RESULT 11

Q9UL75 PRELIMINARY; PRT; 122 AA.

ID AC Q9UL75;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment)  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=98271139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035039; AAC56275.1; -;  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1 1  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Alignment Scores:  
Pred. No.: 1.26e-28 Length: 122  
Score: 363.50 Matches: 75  
Percent Similarity: 73.77% Conservative: 15  
Best Local Similarity: 61.48% Mismatches: 25  
Query Match: 48.92% Indels: 7  
DB: 4 Gaps: 3

US-08-728-463B-205 (1-403) x Q9UL75 (1-122)

Qy 58 CAGGTGCAGCTACAGACTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTC 117  
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuVallysProSerGlnThrLeuSerLeu 20  
Qy 118 ACTCGCGTGCTATGTTGGGTCTTCAGT-----GGTTACTCGAGCTCGATCCGC 171  
Db 21 ThrCysAlaIleSerGlyAspSerValSerAsnSerAlaIleTrpAsnTrpIleArg 40  
Qy 172 CAGCCCCCAGGTAAAGGGCTCGAGTGGATTGGGAAAATACTCATGTGGAAGC----- 225  
Db 41 GlnSerProSerArgGlyLeuGluTrpLeuGlyArgThrTyTyrArgSerLysTrpTyr 60  
Qy 226 ACAACTACAACCCCTCCCTCAAGAGTCGAGTACCATATTCAGTCGACAGCTCAAGAAC 295  
Db 61 AsnAspTyArgValSerVallysSerArgIleThrIleAsnProAspThrSerLysAsn 80  
Qy 286 CAGTTCCTCCCTCAAGCTAGCTCTGTGACGCCCGCACGGCTGTGTATTACTGTGCG 345  
Db 81 GlnPheSerLeuGlnLeuAsnSerValThrProGluAspThrAlaValTyTyrCysAla 100  
Qy 346 AGA-----GTAATTAATTTGGTTTCAGCCCTCGGGCCAGGAAACCTGGTCACCGTC 396  
Db 101 ArgAspLeuGluLeuLeuGlyGlnPheAspTyTrpGlyGlnGlyThrLeuValThrVal 120  
Qy 397 TCCTCA 402  
Db ::::|

```

Db      1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY      61 GTGACGCTACAGCAGTGGGGCGCAGGACTGTGTGAAGCCTTCGGAGACCTGTCTCCCTACC 120
Db      21 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysSerSerGluThrLeuSerLeuThr 40
QY      121 TCCGCTGTCTATGGTGGCTCTTC-----AGTGGTGTACTACTGGAGCTGGATCCGCCAG 174
Db      41 CysThrValSerGlyGlySerIleSerSerSerSerSerSerSerSerSerSerSerSerSer 60
QY      175 CCCCAGCTAAGGGGCTCGAGTGGATTCGGGAATCAATCATAGTGGAGACCACTAC 234
Db      61 ProProGlyLysGlyLeuGluTrpIleAlaSerThrTyThrSerGlyIleThrTyThr 80
QY      235 AACCGCTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCAGAGAACCACTCTCC 294
Db      81 AenProSerLeuLysSerArgValThrIleSerValAspThrSerLysAenGlnLeuSer 100
QY      295 CTGAAGCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGGAGA----- 348
Db      101 LeuLysValArgSerValThrAlaAlaAspThrAlaValTyPheCysAlaArgHisGly 120
QY      349 -----GTAATTAATTGGTTCCACCCCTGGGCGCAGGAAACCTGTCCACC 393
Db      121 TyrSerArgSerGlyArgThrGlyAlaIleAspTyThrGlyGlnGlyThrLeuValThr 140
QY      394 GTCTCTCTCA 402
Db      141 ValSerSer 143

```

## RESULT 8

```

ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0B CRC64;

```

## Alignment Scores:

```

Pred. No.: 1.19e-41 Length: 119
Score: 491.00 Matches: 95
Percent Similarity: 85.71% Conservative: 7
Best Local Similarity: 79.83% Mismatches: 13
Query Match: 66.08% Indels: 4
DB: 4 Gaps: 1

```

US-08-728-463b-205 (1-403) x Q9UL73 (1-119)

```

QY      58 CAGGTGACGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCTCCCTC 117

```

```

Db      1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20
QY      118 ACCTGGCGCTCTATGGTGGCTCTTCAGTGGTACTACTGGAGCTGGATCCGCCAGCCC 177
Db      21 ThrCysThrValSerGlyGlySerIleCysSerSerTyThrSerTrpIleArgGlnPro 40
QY      178 CCAGGTAAGGGGCTCGAGTGGATTCGGGAATCAATCATAGTGGAGACCACTACAAC 237
Db      41 ProGlyLysGlyLeuGluTrpIleGlyTyThrTyThrSerGlySerThrAenTyThr 60
QY      238 CCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACACCTCCAGAGAACCACTCTCCCTG 297
Db      61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAenGlnPheSerLeu 80
QY      298 AACCTGAGCTCTGTGACCGCGCGGACACGGCTGTGTATTACTGTGGAGAGTAATAAT 357
Db      81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyPheCysAlaArgLeuSerAen 100
QY      358 TGG-----TTCGACCCCTGGGCGCAGGAAACCTGTCTACCCCTCTCTCA 402
Db      101 TrpGlyProTyThrPheAspTyThrGlyGlnGlyThrLeuValThrValSerSer 119

```

## RESULT 9

```

ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

```

## Alignment Scores:

```

Pred. No.: 1.75e-41 Length: 473
Score: 490.50 Matches: 97
Percent Similarity: 78.93% Conservative: 12
Best Local Similarity: 70.29% Mismatches: 24
Query Match: 66.02% Indels: 5
DB: 4 Gaps: 2

```

US-08-728-463b-205 (1-403) x Q8TC63 (1-473)

```

QY      1 ATGAACACCTGTGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCAG 60
Db      8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerArg 27
QY      61 GTGACGCTACAGCAGTGGGGCGCAGGACTGTGTGAAGCCTTCGGAGACCTGTCTCCCTACC 120
Db      28 LeuGlnLeuGlnGluSerGlyProGlyLeuLysProSerValThrLeuSerLeuThr 47
QY      121 TCCGCTGTCTATGGTGGCTCTTC-----AGTGGTGTACTACTGGAGCTGGATCCGCCAG 174
Db      48 CysThrValSerGlyAspSerValAlaSerSerSerTyThrTyThrGlyTrpValArgGln 67
QY      175 CCCCAGCTAAGGGGCTCGAGTGGATTCGGGAATCAATCATAGTGGAGACCACTAC 234
Db      68 ProProGlyLysGlyLeuGluTrpIleGlyThrIleAenPheSerGlyAenMetTyThr 87
QY      235 AACCGCTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCAGAGAACCACTCTCC 294
Db      88 SerProSerLeuArgSerArgValThrMetSerAlaAspMetSerGlyAenSerPheTy 107

```









GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 35.7747 Seconds  
(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-205

Perfect score: 743

Sequence: 1 ATGAACACCTGTGGTCTT .....CTGGTCACCTCCTCTCAG 403

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO\_spool/US08728463/runat\_03062003\_085614\_16815/app\_query.fasta\_1.3690  
-DB=SPTRMBL\_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CNG 1.1.380 -runat\_03062003\_085614\_16815 -NCPU=6 -ICPU=3  
-NO MAP -LARGESQUERY -NEG SCORE=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -DELOP=6 -DELEXT=7  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	87.3	588	4 Q8WUX4	Q8wux4 homo sapien

2	649	87.3	597	4	Q9BU10	Q9bu10 homo sapien
3	649	87.3	618	4	Q96AA6	Q96aa6 homo sapien
4	643	86.5	597	4	Q9BOB8	Q9bob8 homo sapien
5	573.5	77.2	613	4	Q96EY0	Q96ey0 homo sapien
6	553.5	74.5	150	4	Q95973	Q95973 homo sapien
7	524.5	70.6	496	4	Q96KX8	Q96kx8 homo sapien
8	491	66.1	119	4	Q9UL73	Q9ul73 homo sapien
9	490.5	66.0	473	4	Q8TC63	Q8tc63 homo sapien
10	430.5	57.9	479	11	Q99M22	Q99m22 mus musculus
11	363.5	48.9	122	4	Q9UL75	Q9ul75 homo sapien
12	355.5	47.8	482	11	Q91X92	Q91x92 mus musculus
13	353.5	47.6	613	11	Q8VCX7	Q8vcx7 mus musculus
14	343	46.2	298	11	Q9QYF0	Q9qyf0 mus musculus
15	336	45.2	168	11	Q8VDC9	Q8vdc9 mus musculus
16	330	44.4	473	11	Q9D8L4	Q9d8l4 mus musculus
17	326.5	43.9	613	4	Q8WUK1	Q8wuk1 homo sapien
18	323	43.5	140	11	Q924P8	Q924p8 mus musculus
19	322.5	43.4	278	11	Q921K1	Q921k1 mus musculus
20	316.5	42.6	471	4	Q8TC77	Q8tc77 homo sapien
21	314.5	42.3	494	4	Q96K68	Q96k68 homo sapien
22	313.5	42.2	121	11	Q9SNG4	Q9sng4 mus musculus
23	313.5	42.2	145	11	Q924R3	Q924r3 mus musculus
24	313	42.1	597	4	Q96BB9	Q96bb9 homo sapien
25	312	42.0	142	11	Q924Q1	Q924q1 mus musculus
26	311	41.9	118	4	Q9UL74	Q9ul74 homo sapien
27	310.5	41.8	488	11	Q91WR1	Q91wr1 mus musculus
28	310	41.7	146	11	Q924Q8	Q924q8 mus musculus
29	309.5	41.7	143	11	Q924Q5	Q924q5 mus musculus
30	309.5	41.7	143	11	Q924Q0	Q924q0 mus musculus
31	309.5	41.7	145	11	Q924Q7	Q924q7 mus musculus
32	309	41.6	146	11	Q924R8	Q924r8 mus musculus
33	308.5	41.5	143	11	Q924R7	Q924r7 mus musculus
34	308.5	41.5	143	11	Q91VA2	Q91va2 mus musculus
35	308.5	41.5	143	11	Q91V67	Q91v67 mus musculus
36	307.5	41.4	463	11	Q93LC4	Q93lc4 mus musculus
37	307	41.3	489	11	Q9VCX4	Q9vcx4 mus musculus
38	307	41.3	497	4	Q8WY24	Q8wy24 homo sapien
39	306.5	41.3	143	11	Q924P9	Q924p9 mus musculus
40	306.5	41.3	573	4	Q8WU38	Q8wu38 homo sapien
41	305	41.0	140	11	Q924R2	Q924r2 mus musculus
42	304.5	41.0	137	11	Q924R6	Q924r6 mus musculus
43	304.5	41.0	143	11	Q924R0	Q924r0 mus musculus
44	304	40.9	119	4	Q9UL94	Q9ul94 homo sapien
45	303	40.8	113	4	Q9UL90	Q9ul90 homo sapien

#### ALIGNMENTS

RESULT 1  
Q8WUX4 PRELIMINARY; PRT; 588 AA.  
ID Q8WUX4;  
AC Q8WUX4;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Hypothetical 64.4 kDa protein.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUES=LYMPH;  
RA Strausberg R.;  
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAH19235.1; --  
DR InterPro; IPR003599; IG\_--  
DR InterPro; IPR003597; IG\_--  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG\_5.  
DR SMART; SM00409; IG\_2.  
DR SMART; SM00407; IGc1; 4.

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 17.1229 Seconds

(without alignments)  
4764.744 Million cell updates/sec

Title: US-08-728-463B-205

Perfect score: 743

Sequence: 1 ATGAACACTGTGGTCTT.....CTGGTCACCGTCTCTCTAG 403

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DBV=xlp  
-Q=/cgn2\_1/USPTO spool/US08728463/runat\_03062003\_085618\_16959/app.query.fasta\_1.3690  
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USERS=US08728463 @CGN 1 1 51 @runat\_03062003\_085618\_16959  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pcp:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	79.2	249	9 US-09-880-748-1321	Sequence 1321, Ap
2	555.5	74.8	249	9 US-09-880-748-957	Sequence 957, App
3	551	74.2	476	9 US-10-124-905-12	Sequence 12, Appl
4	551	74.2	476	9 US-09-948-4298-12	Sequence 12, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-880-748-1321  
; Sequence 1321, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys

; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1321  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1321

5 548.5 73.8 487. 10 US-09-880-729-145 Sequence 145, App  
6 543 73.1 255 9 US-09-880-748-1642 Sequence 1642, Ap  
7 540 72.7 253 9 US-09-880-748-1333 Sequence 1333, Ap  
8 539.5 72.6 254 9 US-09-880-748-1659 Sequence 1659, Ap  
9 535.5 72.1 250 9 US-09-880-748-1413 Sequence 1413, Ap  
10 534 71.9 467 9 US-10-211-357-8 Sequence 8, Appli  
11 534 71.9 467 9 US-10-211-357-10 Sequence 10, Appl  
12 534 71.9 467 9 US-10-211-357-12 Sequence 12, Appl  
13 534 71.9 476 9 US-10-124-905-4 Sequence 4, Appli  
14 534 71.9 476 9 US-09-948-4298-4 Sequence 4, Appli  
15 530 71.3 117 10 US-09-864-761-44315 Sequence 44315, A  
16 530 71.3 139 9 US-10-211-357-2 Sequence 2, Appli  
17 530 71.3 139 10 US-09-850-165-17 Sequence 17, Appl  
18 523.5 70.5 252 9 US-09-880-748-1326 Sequence 1326, Ap  
19 518 69.7 97 9 US-10-194-975-40 Sequence 40, Appl  
20 515 69.3 250 9 US-09-880-748-993 Sequence 993, App  
21 512 68.9 253 9 US-09-880-748-954 Sequence 954, App  
22 511.5 68.8 251 9 US-09-880-748-1316 Sequence 1316, Ap  
23 509 68.5 97 9 US-10-194-975-49 Sequence 49, Appl  
24 505 68.0 253 9 US-09-880-748-1602 Sequence 1602, Ap  
25 504 67.8 255 9 US-09-880-748-1626 Sequence 1626, Ap  
26 495.5 66.7 250 9 US-09-880-748-1645 Sequence 1645, Ap  
27 494 66.5 119 9 US-10-125-687-5 Sequence 5, Appli  
28 494 66.5 119 12 US-10-025-687-5 Sequence 5, Appli  
29 486.5 65.5 254 9 US-09-880-748-1578 Sequence 1578, Ap  
30 485.5 65.3 250 9 US-09-880-748-1548 Sequence 1548, Ap  
31 472.5 63.6 252 9 US-09-880-748-1329 Sequence 1329, Ap  
32 471 63.4 130 9 US-09-925-299-971 Sequence 971, App  
33 471 63.4 130 10 US-09-925-299-971 Sequence 971, App  
34 468 63.0 253 9 US-09-880-748-1339 Sequence 1339, Ap  
35 466.5 62.8 248 9 US-09-880-748-1360 Sequence 1360, Ap  
36 464 62.4 251 9 US-09-880-748-990 Sequence 990, App  
37 463 62.3 97 9 US-10-194-975-50 Sequence 50, Appl  
38 461 62.0 253 9 US-09-880-748-1619 Sequence 1619, Ap  
39 461 62.0 255 9 US-09-880-748-841 Sequence 841, App  
40 460.5 62.0 256 9 US-09-880-748-1607 Sequence 1607, Ap  
41 459 61.8 105 10 US-09-864-761-44573 Sequence 44573, A  
42 457.5 61.6 119 9 US-10-078-958-3 Sequence 3, Appl  
43 457.5 61.6 247 9 US-09-880-748-1651 Sequence 1651, Ap  
44 453.5 61.0 244 12 US-10-039-785-44 Sequence 44, Appl  
45 450.5 60.6 252 9 US-09-880-748-1994 Sequence 1994, Ap

Alignment Scores:

1.23e-46	Length:	249
598.50	Matches:	112
89.6%	Conservative:	1
88.8%	Mismatches:	2
79.21%	Indels:	11
9	Gaps:	11
DB:		

US-08-728-463B-205 (1-403) x US-09-880-748-1321 (1-249)

58	CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTGAAGCCTTCGAGAGACCCCTGTCTCCTC	117	QY
1	GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu	20	Db
118	ACCTGCGCTGCTATGTTGGTCCCTCAGTGGTTACTACTGGAGCTGGATCGCGCAGCCC	177	QY
21	ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro	40	Db
178	CCAGGTAAAGGGCTCGAGTGGATTGGGGAATCAATCATAGTGAAGCACCACCACTACAC	237	QY
41	ProGlyLysGlyLeuGluTrpIleGlyLulLAsnHisSerGlySerThrAsnTyrAsn	60	Db
238	CCGTCCCTCAAGAGTCGAGTGCACATATCATGTCGACACGTCCAAGAACAGATTCTCCCTG	297	QY
61	ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu	80	Db
298	AAGTGTAGCTGTGACCGCGCGGACACCGCTGTGTATTACTGTCTCGAGA	348	QY
81	LysLeuSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGlyProArg	100	Db
349	-----GTAATAATTTGGTTTCACCCCTGGGGCCAGGGAACC	384	QY
101	TyrTyrAspIleLeuThrGlyTyrArgTyrAsnTrpPheAspProTrpGlyArgGlyThr	120	Db
385	CTGTGTCACCGTCTCCTCA	402	QY
121	LeuValThrValSerSer	126	Db

## RESULT 2

US-09-880-748-957  
; Sequence 957, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:

**Alignment Scores:**

Pred. No.:	1.45-43	Length:	249
Score:	555.50	Matches:	107
Percent Similarity:	88.1%	Conservative:	4
Best Local Similarity:	84.92%	Mismatches:	11
Query Match:	74.76%	Indels:	1
DB:	9	Gaps:	1

US-08-728-463B-205 (1-403) x US-09-880-748-957 (1-249)

58	QY	CAGTGTGACGTACAGCAGTGGGGCGCAGGACTGTGAAGCCTTCGAGAGACCCCTGTCCCTC	117
1	Db	GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu	20
118	QY	ACCTCGCGTCTATGGTGGGTCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGGCC	177
21	Db	ThrCysAlaValTyrGlySerPheSerAsnTyrTyrTrpSerTrpIleArgGlnPro	40
178	QY	CCAGTAAGGGCGCTGGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCACTACAAC	237
41	Db	ProGlyLysGlyLeuGluTrpValGlyGluIleAsnHisSerGlySerThrAsnTyrAsn	60
238	QY	CCGTCCCTCAAGAGTCAGAGTCAACATATCATAGTCGACACAGTCCAAAGAACAGATTCTCCCTG	297
61	Db	ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu	80
298	QY	AAGCTGAGCTCTGTGACCGCGGGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT	357
81	Db	LysLeuSerValThrAlaAlaAspThrAlaValTyrCysAlaArgValGlyLeu	100
358	QY	TGGTTC-----GACCCCTGGGGCCAGGGGAACC	384
101	Db	TyrTyrAspIleuThrGlyTyrTyrProSerGlyMetAspValTrpGlyLysGlyThr	120
385	QY	CTGCTCACCGTCTCCTCA	402
121	Db	LeuValThrValSerSer	126

## RESULT 3

US-10-124-905-12  
; Sequence 12, Application US/10124905  
; Patent No. US20020166136A1

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/ CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 / STREET: 699 Prince Street  
 / CITY: Alexandria  
 / STATE: VA  
 / COUNTRY: USA  
 / ZIP: 22314

```

/      ZIP: 22314
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/124,905
/ FILING DATE:
/

```

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012713-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-10-124-905-12

Alignment Scores:  
Pred. No.: 4,23e-43 Length: 476  
Score: 551.00 Matches: 111  
Percent Similarity: 81.51% Conservative: 8  
Best Local Similarity: 76.03% Mismatches: 15  
Query Match: 74.16% Indels: 12  
DB: 4 Gaps: 4

US-08-728-463B-205 (1-403) x US-10-124-905-12 (1-476)

QY 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGGAGCTCCAGATGGGTCTGTCTCCAG 60  
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
QY 61 GTGACGCTACAGCAGTGGGGCGGAGGACTGTGAAAGCTTCGGAGACCTGTCTCCAC 120  
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
QY 121 TGGCTGTCTATGGTGGTCTTCTAGT---GGTTACTTGGAGCTGGATCCGCGAGCCC 177  
Db 41 CysAlaValSerGlySerIleSerGlyGlyTrpGlyTrpIleArgGlnPro 60  
QY 178 CAGGTAAGGGCTGTGAGTGGGAGTGGGAAATC---AATCATAGTGGAGCACAACCTAC 234  
Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80  
QY 235 AACCCGTCCCTCAAGAGTCGAGTCACATATCAGTCGACACGTCCTCAAGAACCACTCTCC 294  
Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100  
QY 295 CTGAAGCTGAGCTGTGACCGCGGAGACACGCTGTGTATTACTGTGCGAGA----- 348  
Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg 120  
QY 349 -----GTAATT-----AATTGGTTCGACCCCTGGGCGCAGGGAACC 384  
Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140  
QY 385 CTGGTCACCGTCTCTCTCA 402  
Db 141 LeuValThrValSerSer 146

RESULT 4

US-09-948-429B-12  
Sequence 12, Application US/09948429B  
Patent No. US20020177689A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/948,429B  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-948-429B-12

Alignment Scores:  
Pred. No.: 4,23e-43 Length: 476  
Score: 551.00 Matches: 111  
Percent Similarity: 81.51% Conservative: 8  
Best Local Similarity: 76.03% Mismatches: 15  
Query Match: 74.16% Indels: 12  
DB: 4 Gaps: 4

US-08-728-463B-205 (1-403) x US-09-948-429B-12 (1-476)

QY 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGGAGCTCCAGATGGGTCTGTCTCCAG 60  
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
QY 61 GTGACGCTACAGCAGTGGGGCGGAGGACTGTGAAAGCTTCGGAGACCTGTCTCCAC 120  
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
QY 121 TGGCTGTCTATGGTGGTCTTCTAGT---GGTTACTTGGAGCTGGATCCGCGAGCCC 177  
Db 41 CysAlaValSerGlySerIleSerGlyGlyTrpGlyTrpIleArgGlnPro 60  
QY 178 CAGGTAAGGGCTGTGAGTGGGAAATC---AATCATAGTGGAGCACAACCTAC 234  
Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80  
QY 235 AACCCGTCCCTCAAGAGTCGAGTCACATATCAGTCGACACGTCCTCAAGAACCACTCTCC 294  
Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100  
QY 295 CTGAAGCTGAGCTGTGACCGCGGAGACACGCTGTGTATTACTGTGCGAGA----- 348  
Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg 120  
QY 349 -----GTAATT-----AATTGGTTCGACCCCTGGGCGCAGGGAACC 384  
Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140  
QY 385 CTGGTCACCGTCTCTCTCA 402  
Db 141 LeuValThrValSerSer 146

RESULT 5

US-09-800-729-145  
Sequence 145, Application US/09800729  
Patent No. US20020068319A1  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: 32 Human secreted proteins  
FILE REFERENCE: PZ044P1  
CURRENT APPLICATION NUMBER: US/09/800,729  
CURRENT FILING DATE: 2001-03-08

;; PRIOR APPLICATION NUMBER: PCT/US00/26013  
;; PRIOR FILING DATE: 2000-09-22  
;; PRIOR APPLICATION NUMBER: 60/155,709  
;; PRIOR FILING DATE: 1999-09-24  
;; NUMBER OF SEQ ID NOS: 217  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 145  
;; LENGTH: 487  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-800-729-145

Alignment Scores:  
Pred. No.: 7,26e-43 Length: 487  
Score: 548.50 Matches: 110  
Percent Similarity: 80.95% Conservative: 9  
Best Local Similarity: 74.83% Mismatches: 15  
Query Match: 73.82% Indels: 13  
DB: 10 Gaps: 2

US-08-728-463B-205 (1-403) x US-09-800-729-145 (1-487)

QY 1 ATGAACACCTGTGTTCTCTCTCTGTGTGCGAGTCCAGATGGTCTGTCCAG 60  
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
QY 61 GTGAGCTACAGAGTGGGGCGAGCTGTGTGAAGCTTGGAGACCCCTGTCCCTCAC 120  
Db 21 ValGlnLeuGlnUserGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
QY 121 TGGCTGTCTATGTGGTCTCTCAGT-----CGTTACTACGGAGCTGGATCCCGCAG 174  
Db 41 CysThrValSerGlyGlySerHisLeuSerGlyGlyHisTrpSerTrpIleArgGln 60  
QY 175 CCCCAGGTAAAGGGCTGGAGTGGGGAATCAATCATAGTGAAGCACCACCACTAC 234  
Db 61 HisProGlyLysGlyLeuGluTrpIleGlyTrpSerTrpAsnGlyValThrTrpTyr 80  
QY 235 AACCGTCCCTCAAGAGTCAGTCAGTCCATATCAGTCAGCAGCGTCCAGAACCAAGTCTCC 294  
Db 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPheSer 100  
QY 295 CTGAAGCTGAGCTCTGTGACCGCGGACAGCGCTGTGTATTACTGTGCGAGA----- 348  
Db 101 LeuArgLeuSerValThrAlaAlaAspThrAlaValTrpCysAlaLysAspHis 120  
QY 349 -----GTAATTAAATTGGTTCGACCCCTGGCGCCAGGGA 381  
Db 121 ArgAlaThrArgAspGlyTrpGlnLeuGluTrpArgGlyPheAspTrpGlyGlnGly 140  
QY 382 ACCTGTGTCACCTCTCCTCA 402  
Db 141 IleLeuValThrValSerSer 147

## RESULT 6

US-09-880-748-1642  
; Sequence 1642, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499

;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1642  
;; LENGTH: 255  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-1642

Alignment Scores:  
Pred. No.: 2.12e-42 Length: 255  
Score: 543.00 Matches: 105  
Percent Similarity: 84.50% Conservative: 4  
Best Local Similarity: 81.40% Mismatches: 6  
Query Match: 73.08% Indels: 14  
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1642 (1-255)

QY 58 CAGGTGCAGCTACAGCAGTGGGGCGCAGACTGTGAGCCCTTCGAGACCTGTCCCTC 117  
Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
QY 118 ACTGCGCTGTCTATGTGGTCTCTTCACTGCTGTACTACTGAGCTGGATCCCGCAGCCC 177  
Db 21 ThrCysAlaValTrpGlySerPheSerGlyTrpTyrTrpSerTrpIleArgGlnSer 40  
QY 178 CCAGGTAAAGGGCTGAGTGGGATGGGGAATCAATCATAGTGGAGCACCACCTACAC 237  
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisGlyGlySerThrAsnTrpAsn 60  
QY 238 CCGTCCCTCAAGAGTCAGTCCACCATATCAGTCGACACGTCCAGAACCCAGTTCCTCCCTG 297  
Db 61 ProSerLeuLysSerArgValThrIleSerValAspAlaSerLysAsnGlnPheSerLeu 80  
QY 299 AAGCTGAGCTCTGTGACCGCGCAGCAGCGCTGTGTATTACTGTGCGAGAGTAAATTAAT 357  
Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTrpCysAlaArgGluArgSer 100  
QY 358 TGGTTC-----GACCCCTGGGGC 375  
Db 101 TyrTrpAspIleLeuThrGlyTrpSerProArgSerLysTrpGlyMetAspValTrpGly 120  
QY 376 CAGGAACCTGTGTCACCGTCTCCTCA 402  
Db 121 ArgGlyThrLeuValThrValSerSer 129

## RESULT 7

US-09-880-748-1333  
; Sequence 1333, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1333  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Homo sapiens



US-09-880-748-1333

## Alignment Scores:

Pred. No.: 4,02e-42 Length: 253  
Score: 540.00 Matches: 107  
Percent Similarity: 85.8% Conservative: 2  
Best Local Similarity: 84.2% Mismatches: 6  
Query Match: 72.68% Indels: 12  
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1333 (1-253)

QY 58 CAGGTGACAGTACAGAGTGGGGCGCAGAGCTGTTGAAGCCTTCGGAGACCTGTCCTC 117  
DB 1 GlnValGlnLeuGlnGlnArgGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
QY 118 ACCTGCGCTGTATGTTGGTTCCTTCACTGAGTGGTGTACTGAGTGGATCCGCCAGGCC 177  
DB 21 ThrCysAlaValTyrGlyGluSerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40  
QY 178 CCAGTAAGGGCTGGAGTGGATTGGGAAATCAATCATAGTGGAGCAACCAACTACAAC 237  
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60  
QY 238 CGTCCCTCAAGAGTCGAGTCCACCATATCAGTCGACACGCTCCAAAGACCACTCCCTG 297  
DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80  
QY 298 AAGCTGAGCTCTGTGACCGCGCAGACACGGCTGTATTACTGTGCGAGA----- 348  
DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaPheTyrTyrCysAlaArgGlySerLeu 100  
QY 349 -----GTAATTAATTGTTCTCGACCCCTCGAGCCCTGGGGCCAGGGA 381  
DB 101 TyrTyrAspIleLeuThrGlyTyrTyrIleGlyAsnAlaPheAspIleTrpGlyArgGly 120  
QY 382 ACCCTGGTCACCGTCTCCTCA 402  
DB 121 ThrLeuValThrValSerSer 127

## RESULT 8

US-09-880-748-1659  
; Sequence 1659, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1659  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1659

## Alignment Scores:

Pred. No.: 4,48e-42 Length: 254  
Score: 539.50 Matches: 106  
Percent Similarity: 85.18% Conservative: 3  
Best Local Similarity: 82.81% Mismatches: 6

Query Match: 72.61% Indels: 13  
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1659 (1-254)

QY 58 CAGGTGACAGTACAGAGTGGGGCGCAGAGCTGTTGAAGCCTTCGGAGACCTGTCCTC 117  
DB 1 GlnValGlnLeuGlnGlnSerGlyProGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
QY 118 ACCTGCGCTGTATGTTGGTTCCTTCACTGAGTGGTGTACTGAGTGGATCCGCCAGGCC 177  
DB 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40  
QY 178 CCAGTAAGGGCTGGAGTGGATTGGGAAATCAATCATAGTGGAGCAACCAACTACAAC 237  
DB 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60  
QY 238 CGTCCCTCAAGAGTCGAGTCCACCATATCAGTCGACACGCTCCAAAGACCACTCCCTG 297  
DB 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80  
QY 298 AAGCTGAGCTCTGTGACCGCGCAGACACGGCTGTATTACTGTGCGAGAGTAATTAAT 357  
DB 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyArg 100  
QY 358 TGGTTC-----GACCCCTGGGGCCAG 378  
DB 101 TyrTyrAspIleLeuThrGlyTyrSerLeuGlyArgGlyGluMetAspValTrpGlyArg 120  
QY 379 GGAACCTGGTCACCGTCTCCTCA 402  
DB 121 GlyThrLeuValThrValSerSer 128

## RESULT 9

US-09-880-748-1413  
; Sequence 1413, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1413  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1413

## Alignment Scores:

Pred. No.: 1,05e-41 Length: 250  
Score: 535.50 Matches: 103  
Percent Similarity: 86.29% Conservative: 4  
Best Local Similarity: 83.06% Mismatches: 8  
Query Match: 72.07% Indels: 9  
DB: 9 Gaps: 1

US-08-728-463B-205 (1-403) x US-09-880-748-1413 (1-250)

QY 58 CAGGTGACAGTACAGAGTGGGGCGCAGAGCTGTTGAAGCCTTCGGAGACCTGTCCTC 117  
DB: 9







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; INFORMATION FOR SEQ ID NO: 118:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 116 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;
US-08-545-809A-118

```

Alignment Scores:		
Pred. No.:	4, 018-60	Length:
Score:	622.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	83.71%	Indels:
DB:	3	Gaps:

US-08-728-463B-205 (1-403) x US-08-545-809A-118 (1-116)

1	ATGAAACACCTGTGGTCTTCTCTCTCTGGTGGCAGCTCCAGATGGGTCGTGCTCCAG	60
1	MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln	20
61	GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGAGACCCCTGCTCCAC	120
21	ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr	40
121	TGCGCTGCTATGGTGGGTCTCTCAGTGGTTTACTTACGTGGAGCTGGATCGCCAGCCGCCCA	180
41	CysAlaValTyrGlyGlySerPheSerGlyTyrTrpSerTrpIleArgGlnProPro	60
181	GGTAAAGGGCTCGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCTACAACCCG	240
61	GlyLysGlyLeuGluTrpIleGlyGluIleasnHisSerGlySerThrAsnTyrAsnPro	80
241	TCCCTCAAGAGTCGAGTCACCATATCAGTCGACACGTCCTCAAGAACCCAGTTTCTCCCTGAAG	300
81	SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys	100
301	CTGAGCTCTGTGACCGCCGCGGACACGCTGTGTATTACTGTGCGAGA	348
101	LeuSerSerValThrAlaAlaAspThrAlaValTyrTrpCysAlaArg	116

RESULT 2

US-08-793-450-8  
Sequence 8, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHABAHI, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566

; FILING DATE: 02-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NORMAN F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ;

Alignment Scores:	
Pred. No.:	1,278-56
Score:	592.00
Percent Similarity:	86.67%
Best Local Similarity:	84.4%
Query Match:	79.68%
DB:	4
Length:	472
Matches:	114
Conservative:	3
Mismatches:	10
Indels:	8
Gaps:	1

US-08-728-463B-205 (1-403) x US-08-793-450-8 (1-472)

22	CTCTCTCTGGTGGGAGCTCCAGATGGGTCTCTCCAGTGCAGCTACAGACGTGGGC	81
8	LeuPheLeuValAlaThrAlaThrGlyValHisSerGlnValGlnLeuGluGlnTrpGly	27
82	CGAGGACTGTGAAGCCTTCGGAGACCCTCTCCCTCACCTGCCTCTCTATGGTGGGTCC	141
28	AlaGlyLeuLeuLysProSerGluThrLeuSerLeuThrCysThrValTyrGlyGlySer	47
142	TTCAGTGGTGTACTACTCGAGCTGGATCGGCAGCCGCCAGCTAAGGGCTGGAGTGGATT	201
48	PheSerGlyTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTrpIle	67
202	GGGGAAATCAATCATAGTGGAGACCAACTACAACCCGTCCTCAAGAGTCGAGTCACC	261
68	GlyGluIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerAszValThr	87
262	ATATCAGTTCGACAGTCCAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCCGCGG	321
88	IleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuAsnSerValThrAlaAla	107
322	GACAGGCTGTGTATTACTGTGCCAGTAGTAATT-----AAT	357
108	AspThrAlaValTyrTyrCysAlaArgAlaProGluTyrLysTrpLysTyrHisGlyAsp	127
358	TGGTTCGACCCCTGGGGCAGGGAACCCCTGGTCACCGCTCTCCCTCA	402
128	TroPheAsnProTrpGluGlnGlyThrValThrValSerSer	142

## RESULT 3

US-09-049-672A-4  
Sequence 4, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 9.17299 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

Title: US-08-728-463B-205  
Perfect score: 743  
Sequence: 1 ATGAACACCTGTGTTCTT.....CTGTGTCACCGTCTCTCAG 403

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.\*

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	622	83.7	116	3	US-08-545-809A-118
2	592	79.7	472	4	US-08-793-450-8
3	578.5	77.9	473	4	US-09-049-672A-4
4	578	77.8	123	4	US-08-793-450-4
5	565	76.0	142	2	US-08-480-774A-2
6	551	74.2	476	3	US-08-487-550-12
7	550	74.0	116	3	US-08-545-809A-140
8	539	72.5	118	3	US-08-545-809A-142
9	538	72.4	116	3	US-08-545-809A-92
10	534	71.9	467	4	US-08-523-894-8
11	534	71.9	467	4	US-08-523-894-10
12	534	71.9	467	4	US-08-523-894-12

13	534	71.9	476	3	US-08-487-550-4	Sequence 4, Appl
14	530	71.3	134	1	US-08-259-372A-6	Sequence 6, Appl
15	530	71.3	134	1	US-08-468-671-6	Sequence 6, Appl
16	530	71.3	139	1	US-08-478-039-108	Sequence 108, App
17	530	71.3	139	1	US-08-476-349A-108	Sequence 108, App
18	530	71.3	139	4	US-08-523-894-2	Sequence 2, Appl
19	527	70.9	118	3	US-08-545-809A-123	Sequence 123, App
20	521	70.1	118	3	US-08-545-809A-116	Sequence 116, App
21	514	69.2	120	3	US-08-545-809A-137	Sequence 137, App
22	507.5	68.3	118	4	US-09-025-769B-25	Sequence 25, Appl
23	499.5	67.2	117	3	US-08-545-809A-114	Sequence 114, App
24	494	66.5	119	4	US-09-025-769B-39	Sequence 39, Appl
25	494	66.5	119	4	US-09-025-769B-65	Sequence 65, Appl
26	491.5	66.2	244	4	US-08-918-148-79	Sequence 79, Appl
27	490.5	66.0	119	2	US-08-428-197-16	Sequence 16, Appl
28	490.5	66.0	119	5	PCT-US93-10555-16	Sequence 16, Appl
29	461.5	62.1	122	1	US-08-360-125-11	Sequence 11, Appl
30	461.5	62.1	122	2	US-08-450-578-11	Sequence 11, Appl
31	461.5	62.1	122	2	US-09-017-628-11	Sequence 11, Appl
32	461.5	62.1	122	2	US-09-014-880-11	Sequence 11, Appl
33	461.5	62.1	122	4	US-08-450-363-11	Sequence 11, Appl
34	454	61.1	119	2	US-08-652-818A-10	Sequence 10, Appl
35	451.5	60.8	278	4	US-09-260-527-3	Sequence 3, Appl
36	450.5	60.6	116	1	US-08-478-039-79	Sequence 79, Appl
37	450.5	60.6	116	1	US-08-476-349A-79	Sequence 79, Appl
38	448	60.3	119	1	US-08-360-125-5	Sequence 5, Appl
39	448	60.3	119	2	US-08-450-578-5	Sequence 5, Appl
40	448	60.3	119	2	US-09-017-628-5	Sequence 5, Appl
41	448	60.3	119	2	US-09-014-880-5	Sequence 5, Appl
42	448	60.3	119	4	US-08-450-363-5	Sequence 5, Appl
43	438	59.0	121	1	US-08-478-039-80	Sequence 80, Appl
44	438	59.0	121	1	US-08-476-349A-80	Sequence 80, Appl
45	434.5	58.5	137	2	US-08-621-751A-8	Sequence 8, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-545-809A-118  
; Sequence 118, Application US/08545809A  
; Patent No. 6096878  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; APPLICANT: Matsuda, Fumihiko  
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
; NUMBER OF SEQUENCES: 145  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/545,809A  
; FILING DATE: 27-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP93/00603  
; FILING DATE: 10-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29, 066  
; REFERENCE/DOCKET NUMBER: 06501/004001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154

CONTAINING THE SAME



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STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCYT01
CLONE: 1513264
US-09-049-672A-4

Alignment Scores:
Pred. No.: 3,81e-55 Length: 473
Score: 578.50 Matches: 118
Percent Similarity: 86.01% Conservative: 5
Best Local Similarity: 82.52% Mismatches: 11
Query Match: 77.86% Indels: 9
DB: 4 Gaps: 3

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Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 61 GTCACCTACAGCAGTGGGGCGGAGCTGTTGAAGCCTTCGGAGACCCCTGCCTCACC 120
Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
QY 121 TGGCTGTCTATCGTGGGTCCTTCAGT-----GGTTACTCTGAGCTGGATCCGCCAG 174
Db 41 CysAlaValSerGlySerIleThrSerGlyGlyTrpTrpSerTrpIleArgGln 60
QY 175 CCCCAGGTAAAGGGCTGAGTGGATTGGGGAATCAATCATAGTGGGAAGCACTAC 234
Db 61 ProProGlyLysGlyLeuGlnTrpIleGlyTyrlleTyrlleTyrlleSerGlySerThrLeuTrp 80
QY 235 AACCCGTCCCTCAAGAGTGGAGTACCATATCAGTCGACACGTCGAAGACACGTTCTCC 294
Db 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100
QY 295 CTGAAGCTGAGCTCTGTGACCGCGGACACGGCTGTGATTACTGTGCGAGAGTAATT 354
Db 101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTrpTrpCysAlaArgAsp 120
QY 355 -----AATTGG-----TTCGACCCCTGGGCGGAGGAAACCCCTGGTCACC 393
Db 121 ValGlyLeuArgGlyGlyAsnTrpGlyMetAspValTrpGlyGlnGlyThrLeuValThr 140
QY 394 GTCTCTCA 402
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Db 141 ValSerSer 143
RESULT 4
US-08-793-450-4
Sequence 4, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLSCULE TYPE: protein
US-08-793-450-4

Alignment Scores:
Pred. No.: 2,68e-55 Length: 123
Score: 578.00 Matches: 109
Percent Similarity: 90.24% Conservative: 2
Best Local Similarity: 88.62% Mismatches: 4
Query Match: 77.79% Indels: 8
DB: 4 Gaps: 1

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Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLysProSerGluThrLeuSerLeu 20
QY 118 ACCTCGCTGTCTATCGTGGGTCCTTCAGTGGTACTACTGAGCTGGATCCGCCAGCCC 177
Db 21 ThrCysThrValTyrlleGlySerPheSerGlyTyrlleTrpSerTrpIleArgGlnPro 40
QY 178 CCAGGTAAAGGGCTGAGTGGATTGGGAAATCAATCATAGTGGAGACCACTACAAC 237
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTrpAsn 60
QY 238 CCGTCCCTCAAGAGTGGAGTACCATATCAGTCGACACGTCGAAGAACCCAGTTCTCCCTG 297
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; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
;
; INFORMATION FOR SEQ ID NO: 142:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 118 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
; US-08-545-809A-142
;
; Alignment Scores:
; Pred. No.: 4,91e-51      Length: 118
; Score: 539.00           Matches: 105
; Percent Similarity: 91.53%      Conservative: 3
; Best Local Similarity: 88.98%      Mismatches: 8
; Query Match: 72.54%           Indels: 2
; DB: 3                    Gaps: 1
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; Db 1 MetLysHisLeuTrpPheLeuLeuValAlaProArgTrpValLeuSerGln 20
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; QY 61 GTGCAGCTACAGAGTGGGCGGAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
; Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
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; QY 121 TGGCGTGTCTATGGTGGTCTTCAGTGGTGTCTTACTGAGCTGGATCCGAGCCG 174
; Db 41 CysThrValSerGlySerValSerGlySerTyTrpTrpSerTrpPileArgGln 60
;
; QY 175 CCCCAGGTAAAGGCTGGAGTGGATTTGGGAAATCAATCATAGTGAAGACCAACTAC 234
; Db 61 ProProGlyLysGlyLeuGluTrpPileGlyTyTrpSerGlySerThrAsnTyr 80
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; QY 235 ACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCAAAGACAGTTC 294
; Db 81 AsnProSerLeuLysSerArgValThrLeuSerValAspThrSerLysAsnGlnPheSer 100
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; QY 295 CTGAAGCTGAGCTGTGTGACCCCGGACGCTGTGTATTACTGTGCCAGA 348
; Db 101 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArg 118
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; RESULT 9
;
; US-08-545-809A-92
;   Sequence 92, Application US/08545809A
;   Patent No. 6096878
;   GENERAL INFORMATION:
;     APPLICANT: Honjo, Tesuku
;     APPLICANT: Matsuda, Fumihiko
;     TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;     TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;     NUMBER OF SEQUENCES: 145
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Fish & Richardson, P.C.
;       STREET: 225 Franklin Street
;       CITY: Boston
;       STATE: MA
;       COUNTRY: US
;
; US-08-545-809A-92
;   Sequence 92, Application US/08545809A
;   Patent No. 6136310
;   GENERAL INFORMATION:
;     APPLICANT: Hanna, Nabil
;     APPLICANT: Newman, Roland A.
;     APPLICANT: Reiff, Mitchell E.
;     TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;     TITLE OF INVENTION: Therapy
;     NUMBER OF SEQUENCES: 59
;
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/545,809A
;   FILING DATE: 27-MAR-1996
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/JP93/00603
;   FILING DATE: 10-MAY-1993
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Freeman, John W.
;   REGISTRATION NUMBER: 29,066
;   REFERENCE/DOCKET NUMBER: 06501/004001
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-542-5070
;   TELEFAX: 617-542-8906
;   TELEX: 200154
;
; INFORMATION FOR SEQ ID NO: 92:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 116 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
; US-08-545-809A-92
;
; Alignment Scores:
; Pred. No.: 6,28e-51      Length: 116
; Score: 538.00           Matches: 103
; Percent Similarity: 91.38%      Conservative: 3
; Best Local Similarity: 88.79%      Mismatches: 10
; Query Match: 72.41%           Indels: 0
; DB: 3                    Gaps: 0
;
; US-08-728-463B-205 (1-403) x US-08-545-809A-92 (1-116)
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; Db 1 MetLysHisLeuTrpPheLeuLeuValAlaProArgTrpValLeuSerGln 20
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; QY 61 GTGCAGCTACAGAGTGGGCGGAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
; Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40
;
; QY 121 TGGCGTGTCTATGGTGGTCTTCAGTGGTGTCTTACTGAGCTGGATCCGAGCCG 180
; Db 41 CysThrValSerGlySerLeuSerTyTrpTrpSerTrpPileArgGlnProAla 60
;
; QY 181 GGTAAAGGCTGGAGTGGATTTGGGAAATCAATCATAGTGAAGACCAACTACAAACCG 240
; Db 61 GlyLysGlyLeuGluTrpPileGlyArgIleTyThrSerGlySerThrAsnTyrAsnPro 80
;
; QY 241 TCCTCAAGAGTCGAGTCACCATATCAGTCGACAGCTCCAAAGACAGTTCCTCCTGAAG 300
; Db 81 SerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeuLys 100
;
; QY 301 CTGAGCTGTGTGACCCCGGACGCTGTGTATTACTGTGCCAGA 348
; Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArg 116
;
; RESULT 10
;
; US-08-523-894-8
;   Sequence 8, Application US/08523894
;   Patent No. 6136310
;   GENERAL INFORMATION:
;     APPLICANT: Hanna, Nabil
;     APPLICANT: Newman, Roland A.
;     APPLICANT: Reiff, Mitchell E.
;     TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
;     TITLE OF INVENTION: Therapy
;     NUMBER OF SEQUENCES: 59

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QY 178 CAGGTAAGGGCTGAGTGGATTGGGGAATCAATCATAGTGA---AGCAACACTAC 234
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Db 61 ProGlyArgGlyLeuGluTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 235 AACCCGTCCTCAAGAGTCGAGTCACCATATCATGTCGACACGTCACCAAGACCAAGTCTCC 294
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 295 CTGAAGCTGAGCTCTGACCGCGCGGACACGGCTGTGTATTACTGTGCGAGA----- 348
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrCysAlaArgGlyPro 120
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QY 349 -----GTAAATTAATGTTGACCCCTCGACCCCTGGGCGCCAGGAACC 384
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ArgProAspCysThrThrIleCysTyrGlyTrpValAspValTrpGlyProGlyAsp 140
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QY 385 CTGCTCACCCTCTCCCTCA 402
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 141 LeuValThrValSerSer 146
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-08-259-372A-6
; Sequence 6, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-6
Alignment Scores:
Pred. No.: 4,978-50 Length: 134
Score: 530.00 Matches: 99
Percent Similarity: 84.21% Conservative: 13
Best Local Similarity: 74.44% Mismatches: 21
Query Match: 71.33% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-205 (1-403) x US-08-259-372A-6 (1-134)
QY 1 ATGAACACCTCTGTTCTTCTCTCTCTGTTGGAGCTCCAGATGGGTCTGTCTCCAG 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaValProArgTrpValValSerGln 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GTCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCCTGTCCTCACC 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 ValGlnLeuGlnLysSerGlyProGlyLeuValLysAlaAlaGluThrLeuSerLeuThr 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 TCGCTGCTCTATGTTGGTCTTCTAGTGTGTTACTACTGAGAGTCCGCCAGCCCCCA 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 41 CysThrValSerArgGlySerPheSerAspTyrPheTrpAsnTrpPheArgGlnProAla 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 GGTAGGGGCTGAGTGGATTGGGGAATCAATCATAGTGGAGCACCACCTACACCCG 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GlyLysArgLeuGluTrpLeuGlyArgValTyrThrSerGlySerValAspTyrAsnPro 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 TCCCTCAAGAGTCGAGTCACCATATCATGTCGACAGCTCCCAAGAACAGTTCTCCCTGAAG 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SerLeuLysSerArgValThrValSerValAspThrSerLysLysGlnPheSerLeuArg 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 CTGAGCTGTGACCCCGCGACACGGCTGTGTATTACTGTGCGAGAGATAATTAATGG 360
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 101 LeuSerSerValThrValAlaAspThrAlaValTyrCysAlaArgGlyLeuSerGly 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 TTCGACCCCTGGGGCGCAGGACCCCTGTCACCGTCTCC 399
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 PheAspTyrTrpGlyGlnGlyAlaLeuValThrValSer 133
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-08-468-671-6
; Sequence 6, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
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FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/192,754  
FILING DATE: 11-MAY-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-671-6

Alignment Scores:  
Pred. No.: 4,97e-50 Length: 134  
Score: 530.00 Matches: 99  
Percent Similarity: 84.21% Conservative: 13  
Best Local Similarity: 74.44% Mismatches: 21  
Query Match: 71.33% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-205 (1-403) x US-08-468-671-6 (1-134)

```
QY . 1 ATGAACACCTGTGTTCTTCTCTCTGTGGCAGCTCCAGATGGTCTGTCCAG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   1 MetLysHisLeuTyrPhePheLeuLeuValAlaValProArgTyrValValSerGln 20

QY 61 GTGCAGCTACAGCAGTGGGGCGGAGGACTGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysAlaAlaGluThrLeuSerLeuThr 40

QY 121 TGCCTCTCTATGTGGTCTCTTCAGTGGTCTTACTCTGAGCTGGATCCGAGCCCCCA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   41 CysThrValSerArgGlySerPheSerAspTyrPheTyrPheArgGlnProAla 60

QY 181 GGTAAGGGCTGAGTGGATTGGGGAATCAATAGTGAAGCACCACCACTACAACCCG 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   61 GlyLysArgLeuGluTyrPheGlyArgValTyrThrSerGlySerValAspTyrAsnPro 80

QY 241 TCCTCAAGAGTCGAGTCACCATATCAGTCGACAGTCCAAAGAACAGTTCCTCCGTAAG 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   81 SerLeuLysSerArgValThrValSerValAspThrSerLysGlnPheSerLeuArg 100

QY 301 CTGAGCTCTGTGACCGCGGACAGCGCTGTATTACTGTGCGAGAGTAATTAATTGG 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   101 LeuSerSerValThrValAlaAspThrAlaValTyrTyrCysAlaArgGlyLeuSerGly 120

QY 361 TTGACCCCTGGGGCAGGAACCTGGTCACCGTCTCC 399
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   121 PheAspTyrTrpGlyGlnGlyAlaLeuValThrValSer 133
```

Search completed: June 3, 2003, 09:47:23  
Job time: 12.173 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 16.412 Seconds  
(without alignments)  
4545.477 Million cell updates/sec

Title: US-08-728-463B-206  
 Perfect score: 698  
 Sequence: 1 ATGACATGATGGTCCCGC.....GACCAAGCTGGAGATCAAAC 388

Scoring table: BLOSUM62	
Xgapop	10.0, Xgapext 0.5
Ygapop	10.0, Ygapext 0.5
Fgapop	6.0, Fgapext 7.0
Delop	6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2.1/USPto.spool/US08728463/runat_03062003_085615_16827/app.query.fasta_1.3690
-D=PIR_73 -QFMT=fastan -SUFFIX=xpr -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=516 -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ex -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463@cgn.1.177/runat_03062003_085615_16827 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEVTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	592	84.8	130	2	S40368	IG kappa chain - h
2	591	84.7	117	2	S21527	IG kappa chain pre
3	590	84.5	125	2	S40333	IG kappa chain V-J
4	574	82.2	132	2	S40334	IG kappa chain - h
5	573	82.1	125	2	S40316	IG kappa chain - h
6	571	81.8	129	2	S40369	IG kappa chain - h
7	569	81.5	117	2	S46376	IG kappa chain V-J
8	567	81.2	127	2	S11240	IG kappa chain V r
9	567	81.2	127	2	S40367	IG kappa chain V-J
10	564	80.8	129	2	S52793	IG kappa chain V r
11	563	80.7	132	2	S38646	IG kappa chain V r
12	562	80.5	123	2	S40331	IG kappa chain - h
13	560	80.2	129	1	K1HUKK	IG kappa chain pre
14	560	80.2	141	2	A49134	IG kappa chain V-I

15	559	80.1	125	2	S40349	IG kappa chain V-r
16	557	79.8	128	2	S46372	IG light chain var
17	557	79.8	131	2	S40352	IG kappa chain V-J
18	556	79.7	129	2	S52789	IG kappa chain V-r
19	553.5	79.3	124	2	S40336	IG kappa chain V-J
20	552	79.1	129	2	S40317	IG kappa chain - h
21	546	78.2	129	2	S52792	IG kappa chain V-r
22	543	77.8	124	2	S40318	IG kappa chain V-r
23	542	77.7	117	1	K1HUI2	IG kappa chain pre
24	539	77.2	117	2	B21056	IG kappa chain pre
25	537	76.9	117	2	S24206	IG kappa chain V-r
26	537	76.9	123	2	S40313	IG kappa chain V-J
27	534	76.5	117	1	K1HUI1	IG kappa chain pre
28	533	76.4	117	2	S11700	IG kappa chain pre
29	532	76.2	117	2	S41809	IG kappa chain V-r
30	532	76.2	125	2	S40353	IG kappa chain V-J
31	532	76.2	126	2	S40335	IG kappa chain V-J
32	531	76.1	117	2	C21056	IG kappa chain pre
33	527	75.5	117	2	S46371	IG kappa chain V-J
34	526	75.4	135	2	S24320	IG kappa chain pre
35	525	75.2	117	2	S41810	IG kappa chain V-r
36	524	75.1	116	2	A27594	IG kappa chain pre
37	523.5	75.0	125	2	S40332	IG kappa chain - h
38	522.5	74.9	129	2	S40315	IG kappa chain - h
39	521.5	74.7	120	2	S46374	IG kappa chain V-J
40	521	74.6	122	2	S40314	IG kappa chain - h
41	519	74.4	129	1	K1HUI1	IG kappa chain pre
42	517	74.1	117	2	S42264	IG kappa chain V-r
43	515	73.8	122	2	S40370	IG kappa chain - h
44	515	73.8	130	2	P10113	IG kappa chain pre
45	511	73.2	117	2	S42263	IG kappa chain V-r

## ALIGNMENTS

## RESULT 1

S40368  
IG kappa chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S40368  
R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A/Reference number: S40312; MUID:94080891; PMID:8258341  
A/Accession: S40368  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-130 <KLE>  
A/Cross-references: EMBL:X72478; NID:g441424; PID:g441425  
C/Superfamily: immunoglobulin v region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:33-107/Domain: immunoglobulin homology <IMW>

Alignment Scores:	
Pred. No.:	6,78e-45
Score:	592.00
Percent Similarity:	94.32%
Best Local Similarity:	90.32%
Query Match:	84.81%
DB:	2
Length:	130
Matches:	112
Conservative:	5
Mismatches:	7
Indels:	0
Gaps:	0

US-08-728-463B-206 (1-388) x S40368 (1-130)

Qy	16	CCGCGTCAGTCTCTGGGCGCTCCTGCTGCTGCTGCTGGTCTCCAGAGTTCAGATGCCACATCCAG	75
Db	1	ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGln	20
Qy	76	ATGACCCAGTCTCCATCTTCGCGTGTCTCACTCTGTAGGAGACAGAGTCACCATCACTTGT	135
Db	21	MetThrGlnSerProSerSerValSerAlaSerValGlyAspArgValIleIleThrCys	40
Qy	136	CGGCGCAGTTCAGGATATTAGCAGCTGGTGTAGTCTGGTATCAGCATTAACACGGGAAAGCC	195



```
RESULT 4
S40334
ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
C:Accession: S40334
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,71e-43 Length: 132
Score: 574.00 Matches: 107
Percent Similarity: 93.75% Conservative: 13
Best Local Similarity: 83.59% Mismatches: 8
Query Match: 82.23% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-206 (1-388) x S40334 (1-132)

QY 4 GACATGATGCTCCCGCTCAGCTCCGCGGCTCTGCTCTGCTCTCCAGGTTCCAGA 63
Db 1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaArg 20

QY 64 TCGCATCATCAGATGACCCAGTCTCCATCTCCGCTCTGCTCTGCTCTGAGAGACAGATC 123
Db 21 CysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerIleGlyAspArgVal 40

QY 124 ACATCAGTCTGCGCGAGTCAGATATAGCAGCTGTTAGCTGTTAGCTGATCAGCATATAA 183
Db 41 ThrIleThrCysArgAlaSerGlnGlyIleAsnSerTyrLeuAlaTrpTyrGlnGlnlys 60

QY 184 CAGGGAAAGCCCTAAGCTCTGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
Db 61 ProGlyLysAlaProLysLeuLeuIleTyrValAlaSerThrLeuGlnSerGlyValPro 80

QY 244 TCAAGTTCAGCGGAGTCGATCTGGCAGACAGATTTCACTCTCACCATCAGCAGCTGCGAG 303
Db 81 SerArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGln 100

QY 304 CTGAAGATTTGCAACTTACTATTGTCACAGGCTAAATAGTTTCCCGTACACTTTTGGC 363
Db 101 ProGluAspPheAlaSerTyrTyrCysGlnGlnPheAsnSerTyrProPheThrPheGly 120

QY 364 CAGGGACCAAGCTGAGATCAAA 387
Db 121 GlyGlyThrLysValGluIlearg 128

RESULT 5
S40316
ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
C:Accession: S40316
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40316
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72426
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

```
C:Keywords: heterotetramer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3,36e-43 Length: 125
Score: 573.00 Matches: 110
Percent Similarity: 93.44% Conservative: 4
Best Local Similarity: 90.16% Mismatches: 8
Query Match: 82.09% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-206 (1-388) x S40316 (1-125)

QY 22 CAGCTCCTGGGGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 81
Db 1 GlnLeuLeuGlyLeuLeuLeuTrpPheProGlySerArgCysAspIleGlnLeuThr 20

QY 82 CAGTCTCCATCTTCGCTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 141
Db 21 GlnSerProSerSerValSerAlaSerValGlyAspArgValThrIleThrCysArgAla 40

QY 142 AGTCAGGATATTAGCAGCTGGTTAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCT 201
Db 41 SerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProAsn 60

QY 202 CTCCTGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 261
Db 61 LeuLeuIleTyrHisIleSerSerLeuGlnThrGlyValProSerArgPheSerGlySer 80

QY 262 GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 321
Db 81 GlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAlaIle 100

QY 322 TACTATTGTCACAGCTTAATAGTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 381
Db 101 TyrTyrCysGlnGlnAlaAspSerPheProLeuThrPheGlyGlyThrLysValGlu 120

QY 382 ATCAAA 387
Db 121 IleLys 122

RESULT 6
S40369
ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72479; NID:9441426; PIDN:CAAS1147.1; PID:9441427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 5,03e-43 Length: 129
Score: 571.00 Matches: 112
Percent Similarity: 92.19% Conservative: 6
Best Local Similarity: 87.50% Mismatches: 10
Query Match: 81.81% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-206 (1-388) x S40369 (1-129)

QY 4 GACATGATGTTCCCGCTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
Db 1 AspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
```





QY 241 CCATCAAGTTTCAGCGGACAGTCGATCTGGACAGAGATTTCACTCTCACCATCAGCAGCCTG 300  
 Db |||||  
 QY 83 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerCysLeu 102  
 Db |||||  
 QY 301 CAGCCTGAAGATTTGCACACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTT 360  
 Db |||||  
 QY 103 GlnSerGluAspPheAlaThrTyrCysGlnGlnTyrSerTyrProArgThrPhe 122  
 Db |||||  
 QY 361 GCCCAGGGGACCAAGCTGGAGATCAA 387  
 Db |||||  
 QY 123 GlyGlnGlyThrLysValGluIleLys 131  
 Db |||||

## RESULT 12

S40331  
 Ig kappa chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S40331  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40331; MUID:94080891; PMID:8258341  
 A:Accession: S40331  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <KLE>  
 A:Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:32-106/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 3,21e-42 Length: 123  
 Score: 562.00 Matches: 110  
 Percent Similarity: 93.50% Conservative: 5  
 Best Local Similarity: 89.43% Mismatches: 8  
 Query Match: 80.52% Indels: 0  
 DB: 2 Gaps: 0

US-08-728-463B-206 (1-388) x S40331 (1-123)

QY 19 GCTCAGCTCTGGGGCTCTGCTGCTCTGCTCTCCAGTTCCAGATCCGACATCCAGATG 78  
 Db |||||  
 QY 1 AlaglnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCysAspIleGlnMet 20  
 Db |||||  
 QY 79 ACCAGTCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGTCCACATCACTTGTGG 138  
 Db |||||  
 QY 21 ThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArg 40  
 Db |||||  
 QY 139 GCGAGTCAGGATATTAGCAGCTGGTTAGCTGCTGATCAGCATTAACAGCGGAAAGCCCT 198  
 Db |||||  
 QY 41 AlaSerGlnSerIleSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaPro 60  
 Db |||||  
 QY 199 AAGCTCCTGATCTATGCTGATCCAGTTTGCAAAGTGGGCTCCATCAAGTTTCAGCGGC 258  
 Db |||||  
 QY 61 LysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSerGly 80  
 Db |||||  
 QY 259 AGTGGATCTGGGACAGATTCTCCTCAGCATCAGAGCTGAGCTGAGCTTGAAGATTTCGA 318  
 Db |||||  
 QY 81 SerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAla 100  
 Db |||||  
 QY 319 ACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTGGCCAGGGACCAAGCTG 378  
 Db |||||  
 QY 101 ThrTyr-Tyr-CysGlnGlnSerTyrSerThrProArgThrPheGlyGlnGlyThrLysVal 120  
 Db |||||  
 QY 379 GAGATCAA 387  
 Db |||||  
 QY 121 GluIleLys 123  
 Db |||||

## RESULT 13

KIHUWK  
 Ig kappa chain precursor V-I region (Walker) - human

C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 21-Jan-2000  
 C:Accession: A01883  
 R:Klobeck, H.G.; Combratio, G.; Zachau, H.G.  
 Nucleic Acids Res. 12, 6995-7006, 1984  
 A:Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines.  
 A:Reference number: A93534; MUID:85014148; PMID:6091049  
 A:Accession: A01883  
 A:Molecule type: DNA  
 A:Residues: 1-129 <KLO>  
 A:Note: the sequence was determined from the differentiated gene  
 C:Genetics:  
 A:Gene: GDB:IGKV1  
 A:Cross-references: GDB:136264  
 A:Map position: 2p12-2p12  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:1 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>  
 F:23-45/Region: framework 1  
 F:38-112/Domain: immunoglobulin homology <IMM>  
 F:46-56/Region: complementarity-determining 1  
 F:57-71/Region: framework 2  
 F:72-78/Region: complementarity-determining 2  
 F:79-110/Region: complementarity-determining 3  
 F:111-119/Region: complementarity-determining 3  
 F:120-129/Region: framework 4  
 F:45-110/Disulfide bonds: #status predicted

Alignment Scores:  
 Pred. No.: 4,79e-42 Length: 129  
 Score: 560.00 Matches: 111  
 Percent Similarity: 90.70% Conservative: 6  
 Best Local Similarity: 86.05% Mismatches: 12  
 Query Match: 80.23% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KIHUWK (1-129)

QY 1 ATGCAGATGATGTCCTCCCGCTCAGCTCTGGGGCTCTGCTGCTGTTCCCGAGTTCC 60  
 Db |||||  
 QY 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla 20  
 Db |||||  
 QY 61 AGATCGCATCCAGATGACCCAGTCTCCATCTTCGCTGCTGTCATCTGTAGGAGACAGA 120  
 Db |||||  
 QY 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
 Db |||||  
 QY 121 GTCACCATCACTTCTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCTTGATCAGCAT 180  
 Db |||||  
 QY 41 ValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnGln 60  
 Db |||||  
 QY 181 AAACCGGAAAGCCCTCCTAGCTCTGATCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTG 240  
 Db |||||  
 QY 61 LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80  
 Db |||||  
 QY 241 CCATCAAGTTTCAGCGGACAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTG 300  
 Db |||||  
 QY 81 ThrSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
 Db |||||  
 QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT 360  
 Db |||||  
 QY 101 GlnProGluAspSerAlaThrTyrTyr-CysGlnGlnSerTyrSerThrLeuIleThrPhe 120  
 Db |||||  
 QY 361 GCCCAGGGGACCAAGCTGGAGATCAA 387  
 Db |||||  
 QY 121 GlyGlnGlyThrArgLeuGluIleLys 129  
 Db |||||

## RESULT 14

A49134  
 Ig kappa chain V-I region (ISE) - human (fragment)  
 C:Species: Homo sapiens (man)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.35964 Seconds  
(without alignments)  
4373.264 Million cell updates/sec

Title: US-08-728-463B-206  
Perfect score: 698  
Sequence: 1 ATGGACATGATGTCCTCCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DRV=xlp  
-O=/cgn2.1/USPTO\_spool/US08728463/runat\_03062003\_085614\_16804/app\_query.fasta\_1.3690  
-DB=SwissProt 40 -QFMT=faetan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1.1 76 @runat\_03062003\_085614\_16804 -NCPU=3  
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	560	80.2	129	1 KVIW HUMAN	P04431 homo sapien
2	542	77.7	117	1 KVIJ HUMAN	P01602 homo sapien
3	534	76.5	117	1 KVIH HUMAN	P01601 homo sapien
4	519	74.4	129	1 KVIK HUMAN	P04432 homo sapien
5	479	68.6	108	1 KVIS HUMAN	P01611 homo sapien
6	473	67.8	128	1 KVSE MOUSE	P01637 mus musculus
7	467.5	67.0	107	1 KVID HUMAN	P01596 homo sapien
8	467	66.9	108	1 KVIH HUMAN	P01600 homo sapien
9	466	66.8	108	1 KVIH HUMAN	P04430 homo sapien
10	465	66.6	108	1 KVIH HUMAN	P01604 homo sapien
11	464	66.5	108	1 KVIH HUMAN	P01598 homo sapien
12	460	65.9	108	1 KVIH HUMAN	P01607 homo sapien
13	458	65.6	108	1 KVIH HUMAN	P01610 homo sapien
14	457	65.5	108	1 KVIH HUMAN	P01599 homo sapien
15	453	64.9	108	1 KVIH HUMAN	P01594 homo sapien
16	452	64.8	108	1 KVIH HUMAN	P01606 homo sapien
17	448.5	64.3	129	1 KVIH HUMAN	P01636 homo sapien
18	447.5	64.1	129	1 KVIH HUMAN	P01635 homo sapien

19	447	64.0	108	1 KVIH HUMAN	P01597 homo sapien
20	446	63.9	108	1 KVIH HUMAN	P01605 homo sapien
21	445	63.8	108	1 KVIH HUMAN	P01608 homo sapien
22	443	63.5	130	1 KVSG MOUSE	P01639 mus musculus
23	440	63.0	108	1 KVIH HUMAN	P01638 mus musculus
24	440	63.0	108	1 KVIH HUMAN	P01595 homo sapien
25	437.5	62.7	129	1 KVIH HUMAN	P04207 homo sapien
26	437	62.6	108	1 KVIH HUMAN	P01593 homo sapien
27	436	62.5	108	1 KVIH HUMAN	P01603 homo sapien
28	432	61.9	108	1 KVIH HUMAN	P01609 homo sapien
29	430	61.6	115	1 KV5F MOUSE	P01638 mus musculus
30	430	61.6	128	1 KV3K HUMAN	P06311 homo sapien
31	417	59.7	134	1 KV4C HUMAN	P06314 homo sapien
32	414	59.3	115	1 KVIH HUMAN	P04433 homo sapien
33	408.5	58.5	109	1 KVIH HUMAN	P01612 homo sapien
34	406	58.2	131	1 KV3I MOUSE	P01661 mus musculus
35	405	58.0	108	1 KV5K MOUSE	P01644 mus musculus
36	404	57.9	115	1 KV5C MOUSE	P01635 mus musculus
37	402	57.6	117	1 KV5H MOUSE	P01641 mus musculus
38	402	57.6	132	1 KV3F MOUSE	P01658 mus musculus
39	401.5	57.5	116	1 KV3J HUMAN	P04434 homo sapien
40	400	57.3	108	1 KV5L MOUSE	P01645 mus musculus
41	400	57.3	108	1 KV5O MOUSE	P01648 mus musculus
42	400	57.3	108	1 KV5P MOUSE	P01649 mus musculus
43	399.5	57.2	133	1 KV4B HUMAN	P06313 homo sapien
44	397	56.9	108	1 KV5D MOUSE	P01636 mus musculus
45	395	56.6	108	1 KV5M MOUSE	P01646 mus musculus

#### ALIGNMENTS

RESULT 1  
KVIW HUMAN  
ID KVIW HUMAN STANDARD; PRT; 129 AA.  
AC P04431.  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobeck H.G., Combriato G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
lymphoid cell lines are closely related."  
RL Nucleic Acids Res. 12:6995-7006(1984).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; X00965; CAA25477.1; ALT\_TERM.  
DR PIR; A01883; K1HWK.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.









DB: 1 0 Gaps: 0

US-08-728-463B-206 (1-388) x KV1V\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCCATCTCCGTCGTCGATCTGTAGGACAGAGTCAACC 126  
 Db 1 AsplleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186  
 Db 21 IleThrCysArgAlaSerGlnSerValTyraSerValAlaTrpPheGlnGlnLysPro 40  
 QY 187 GGAAGAGCCCTAAGCTCCTGATCTTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCA 246  
 Db 41 GlyLysAlaProGlnValLeuIleTyraAlaSerSerLeuProSerGlyValProSer 60  
 QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCATCTCCACATCAGCAGCTCGAGCCT 306  
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
 QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 Db 81 GluAspPheAlaThrTyTyCysGlnGlnAsnTyriLeThrProThrSerPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAAA 387  
 Db 101 GlyThrArgValGluIleLys 107

RESULT 9  
 KV1V\_HUMAN STANDARD; PRT; 108 AA.  
 AC P04430.  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region BAN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86174817; PubMed=3083240;  
 RA Dulet F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78(1986).  
 DR PIR; A01878; KIHUKU.  
 DR HSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_V.  
 DR SMART; SM00406; Ig; 1.  
 KW Immunoglobulin V region; Amyloid.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Alignment Scores:  
 Pred. No.: 1.56e-41 Length: 108  
 Score: 466.00 Matches: 87  
 Percent Similarity: 92.52% Conservative: 12  
 Best Local Similarity: 81.31% Mismatches: 8  
 Query Match: 66.76% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1V\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCCATCTCCGTCGTCGATCTGTAGGACAGAGTCAACC 126  
 Db 1 AsplleGlnLeuThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186  
 Db 21 IleThrCysArgAlaSerGlnSerValTyraSerValAlaTrpPheGlnGlnLysPro 40  
 QY 187 GGAAGAGCCCTAAGCTCCTGATCTTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCA 246  
 Db 41 GlyLysAlaProGlnValLeuIleTyraAlaSerSerLeuProSerGlyValProSer 60  
 QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCATCTCCACATCAGCAGCTCGAGCCT 306  
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
 QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 Db 81 GluAspPheAlaThrTyTyCysGlnGlnAsnTyriLeThrProThrSerPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAAA 387  
 Db 101 GlyThrArgValGluIleLys 107

RESULT 10  
 KV1L\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01604;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Kue.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79237924; PubMed=112021;  
 RA Eulitz M., Kley H.-P., Zeitler H.-J.;  
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
 sequence of the variable part of a human L-chain of the kappa-type.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01870; KIHUKU.  
 DR HSP; P01607; 1REI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90B4E98 CRC64;

Alignment Scores:  
 Pred. No.: 2e-41 Length: 108  
 Score: 465.00 Matches: 87  
 Percent Similarity: 91.59% Conservative: 11  
 Best Local Similarity: 81.31% Mismatches: 9  
 Query Match: 66.62% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1L\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGCACTCTGTAGGAGACAGAGTCACC 126  
 DB 1 AspIleGlnMetThrGlnSerProSerThrGlnProAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGGCGGAGTCCAGGATATTAGCAGCTGGTACCTGGTATCAGCATRAACCA 186  
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrPheLeuAlaThrPyrGlnGlnLysPro 40  
 QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGGTCCCATCA 246  
 DB 41 GlyLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60  
 QY 247 AGTTTACGGGAGTGGAGTGGAGATTTTCACTCTCACCATCAGCAGCCTGCGAGCCT 306  
 DB 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80  
 QY 307 GAAGATTTTGCACCTTACTTATTCACAGGCTTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 DB 81 AspAspPheAlaThrTyrrCysGlnGlnTyrrSerArgTyrrProTyrrPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAA 387  
 DB 101 GlyThrLysLeuAspIleLys 107

RESULT 11  
 KVIF\_HUMAN  
 ID KVIF\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01598;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region EU.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=71064023; PubMed=5489770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 RT acid sequence of the light chain."  
 RL Biochemistry 9:3155-3161(1970).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds."  
 RL Biochemistry 9:3188-3196(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01866; KIHUEU.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Alignment Scores:

Pred. No.: 2.55e-41

Length: 108

Score: 464.00 Matches: 88  
 Percent Similarity: 91.59% Conservative: 10  
 Best Local Similarity: 82.24% Mismatches: 9  
 Query Match: 66.48% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463b-206 (1-388) x KVIF\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGCACTCTGTAGGAGACAGAGTCACC 126  
 DB 1 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGGCGGAGTCCAGGATATTAGCAGCTGGTACCTGGTATCAGCATRAACCA 186  
 DB 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrPheLeuAlaThrPyrGlnGlnLysPro 40  
 QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGGTCCCATCA 246  
 DB 41 GlyLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60  
 QY 247 AGTTTACGGGAGTGGAGTGGAGATTTTCACTCTCACCATCAGCAGCCTGCGAGCCT 306  
 DB 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80  
 QY 307 GAAGATTTTGCACCTTACTTATTCACAGGCTTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 DB 81 AspAspPheAlaThrTyrrCysGlnGlnTyrrAsnSerAspSerLysMetPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAA 387  
 DB 101 GlyThrLysValGluValLys 107

RESULT 12

KVIF\_HUMAN

ID KVIF\_HUMAN STANDARD; PRT; 108 AA.

AC P01607;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Rei.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=76023758; PubMed=809329;

RA Palm W., Hilschmann N.;

RT "The primary structure of a crystalline monoclonal immunoglobulin

RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation

RT and characterization of the tryptic peptides; the complete amino acid

RT sequence of the protein; a contribution to the elucidation of the

RT three-dimensional structure of antibodies, in particular their

RT combining site.";

RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=76039968; PubMed=1182131;

RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions

RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";

RL Biochemistry 14:4943-4952(1975).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)

CC MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01873; KIHURE.

DR PDB; IREI; 17-FEB-84.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.

KW

DOMAIN 1 23 FRAMEWORK-1.

FT



FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT STRAND 4 7  
 FT STRAND 10 13  
 FT TURN 15 16  
 FT STRAND 19 25  
 FT STRAND 30 31  
 FT TURN 30 30  
 FT STRAND 33 38  
 FT TURN 40 41  
 FT STRAND 45 49  
 FT TURN 50 52  
 FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
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 FT STRAND 102 106  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Alignment Scores:  
 Pred. No.: 6,76e-41 Length: 108  
 Score: 460.00 Matches: 88  
 Percent Similarity: 89.62% Conservative: 7  
 Best Local Similarity: 83.02% Mismatches: 11  
 Query Match: 65.90% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV10\_HUMAN (1-108)

QY 67 GACATCCAGATACCCAGTCTCCATCTCCGTCCTGTCATCTGTAGGAGACAGATCACC 126  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTGTGCGGAGTCAGGATATAGCAGCTGGTACCTGTCATCAGCATAAACC 186  
 Db 21 IleThrCysGlnAlaSerGlnAspIleIleLysrTyLeuAsnTrpTyGlnThrPro 40  
 QY 187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTCCTCATCA 246  
 Db 41 GlyLysAlaProLysLeuLeuIleTyGluAlaSerAsnLeuGlnAlaGlyValPro 60  
 QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCCT 306  
 Db 61 ArgPheSerGlySerGlyThrAspTyThrPheThrIleSerSerLeuGlnPro 80  
 QY 307 GAAGATTTGCACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 Db 81 GluAspIleAlaThrTyTyCysGlnGlnTyGlnSerLeuProTyThrPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATC 384  
 Db 101 GlyThrLysLeuGlnIle 106

RESULT 13

KV10\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV10\_HUMAN  
 AC P01610;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region WEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83273707; PubMed=6410398;  
 RA Goni F., Frangione B.;  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 (protein WEA) with antibody activity against 3,4-pyruvylated  
 galactose in Klebsiella polysaccharides K30 and K33.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
 AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
 WALDENSTROM'S MACROGLOBULINEMIA.

DR PIR; A01876; KIHUWE.  
 DR HSP; P80362; IWL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR Immunoglobulin V region; Monoclonal antibody.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Alignment Scores:  
 Pred. No.: 1.1e-40 Length: 108  
 Score: 458.00 Matches: 88  
 Percent Similarity: 90.65% Conservative: 9  
 Best Local Similarity: 82.24% Mismatches: 10  
 Query Match: 65.62% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x KV1R\_HUMAN (1-108)

QY 67 GACATCCAGATACCCAGTCTCCATCTCCGTCCTGTCATCTGTAGGAGACAGATCACC 126  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTGTGCGGAGTCAGGATATAGCAGCTGGTACCTGTCATCAGCATAAACC 186  
 Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTyGlnGlnLysPro 40  
 QY 187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGTGGGTCCTCATCA 246  
 Db 41 GlyThrAlaProLysArgLeuIleTyGlyAlaThrSerLeuGlnSerGlyValPro 60  
 QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCCT 306  
 Db 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80  
 QY 307 GAAGATTTGCACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 Db 81 GluAspPheAlaThrTyTyCysLeuGlnTySerSerPheProThrPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAA 387  
 Db 101 GlyThrLysValGluValLys 107

RESULT 14

KV1G\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV1G\_HUMAN  
 AC P01599;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region GNL.



Db 81 GluAspIleAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100  
QY 367 GGGACCAAGCTGGAGATCAAA 387  
Db 101 GlyThrLysValGluIleLys 107

Search completed: June 3, 2003, 09:04:03  
Job time : 9.35964 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 34.431 Seconds

(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-206

Perfect score: 698

Sequence: 1 ATGGACATCATGCTCCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=SPTREMBL\_21 -QFWT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CGN\_1.1.380 @runat\_03062003\_085614.16815 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL\_21:  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	481	68.9	108 4 Q9UL77	Q9UL77 homo sapien

2	473	67.8	108 4 Q9UL70	Q9UL70 homo sapien
3	470.5	67.4	107 4 Q96SA9	Q96SA9 homo sapien
4	470	67.3	234 11 Q8R062	Q8R062 mus musculus
5	463	66.3	234 11 Q91WF8	Q91WF8 mus musculus
6	462	66.2	234 11 Q8VCP0	Q8VCP0 mus musculus
7	456	65.3	108 4 Q9UL79	Q9UL79 homo sapien
8	445.5	63.8	107 4 Q9UL81	Q9UL81 homo sapien
9	439	62.9	127 11 Q925S9	Q925S9 mus musculus
10	431	61.7	233 11 Q91WS9	Q91WS9 mus musculus
11	414	59.3	116 4 Q96PF6	Q96PF6 homo sapien
12	402	57.6	214 11 Q9R1A5	Q9R1A5 mus musculus
13	394	56.4	108 4 Q9UL83	Q9UL83 homo sapien
14	393	56.3	109 11 Q920S6	Q920S6 mus musculus
15	392	56.2	298 11 Q9QYF0	Q9QYF0 mus musculus
16	390	55.9	108 11 Q8VIJ0	Q8VIJ0 mus musculus
17	383.5	54.9	239 4 Q8TCD0	Q8TCD0 homo sapien
18	383	54.9	107 11 Q9JL84	Q9JL84 mus musculus
19	382.5	54.8	109 4 Q9UL78	Q9UL78 homo sapien
20	379.5	54.4	109 4 Q9UL85	Q9UL85 homo sapien
21	378	54.2	238 11 Q99M37	Q99M37 mus musculus
22	377	54.0	111 11 Q920S9	Q920S9 mus musculus
23	364.5	52.2	109 4 Q9UL86	Q9UL86 homo sapien
24	362	51.9	238 11 Q8VC16	Q8VC16 mus musculus
25	357.5	51.2	241 11 Q921A6	Q921A6 mus musculus
26	354.5	50.8	134 11 Q8VDD0	Q8VDD0 mus musculus
27	350.5	50.2	239 11 Q8VC55	Q8VC55 mus musculus
28	347	49.7	107 11 Q9ER29	Q9ER29 mus musculus
29	342.5	49.1	106 5 Q9U410	Q9U410 schistosoma
30	340	48.7	234 11 Q8R028	Q8R028 mus musculus
31	337	48.3	99 11 Q9JL74	Q9JL74 mus musculus
32	334	47.9	101 11 Q9JL78	Q9JL78 mus musculus
33	327	46.8	103 11 Q9JL80	Q9JL80 mus musculus
34	321.5	46.1	235 11 Q9JL72	Q9JL72 mus musculus
35	318	45.6	97 11 Q9JL76	Q9JL76 mus musculus
36	305.5	43.8	104 11 Q9JL82	Q9JL82 mus musculus
37	304	43.6	114 4 Q9UL80	Q9UL80 homo sapien
38	294	42.1	109 6 Q9N0W5	Q9N0W5 cryptotlagus
39	265	38.0	130 4 Q8NFP29	Q8NFP29 homo sapien
40	262.5	37.6	233 4 Q8TBC9	Q8TBC9 homo sapien
41	250.5	35.9	237 4 Q8WTU6	Q8WTU6 homo sapien
42	246.5	35.3	237 4 Q8WUK4	Q8WUK4 homo sapien
43	231	33.1	107 4 Q9JL82	Q9JL82 homo sapien
44	230.5	33.0	107 4 Q9NSD6	Q9NSD6 homo sapien
45	225.5	32.3	236 4 Q96E61	Q96E61 homo sapien

## ALIGNMENTS

RESULT 1

Q9UL77 PRELIMINARY; PRT; 108 AA.  
ID Q9UL77  
AC Q9UL77;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
DE (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; RAD56273.1; -  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.









RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035033; AAD56269.1; --  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON\_TER 1 107  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;  
  
 Alignment Scores:  
 Pred. No.: 6.6e-42 Length: 107  
 Score: 445.50 Matches: 89  
 Percent Similarity: 89.72% Conservative: 7  
 Best Local Similarity: 83.18% Mismatches: 10  
 Query Match: 63.83% Indels: 1  
 DB: 4 Gaps: 1  
  
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 QY 67 GACATCCAGATGACCCAGTCCATCTCCGTGTCATCTGTAGGAGACAGTCACC 126  
 Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTCTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGATCAGCATAACCA 186  
 Db 21 IleThrCysArgAlaSerGlnSerIleSerAsnIleLeuAsnTrpThrGlnGlnLysPro 40  
 QY 187 GGGAAACCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCTCATCA 246  
 Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60  
 QY 247 AGGTTTCAGCGGAGTCGATCTGGAGAGATTTCACTCTACCATCAGCAGCTGACGCT 306  
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80  
 QY 307 GAAGATTTTGCACTTACTATTGTCACAGCTTAATAGTTTCCGTCACATCTTTGGCCAG 366  
 Db 81 GluAspPheAlaThrTyrCysGlnGlnSerTyrSer---AlaLeuThrPheGlyPro 99  
 QY 367 GGGACCAAGCTGGAGATCAAA 387  
 Db 100 GlyThrLysValAspIleArg 106

RESULT 9  
 Q925S9 PRELIMINARY; PRT; 127 AA.  
 AC Q925S9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Immunoglobulin light chain (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C;  
 RX MEDLINE=99306687; PubMed=10380019;  
 RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,  
 RA Foon K.A., Chatterjee S.K.;  
 RT "Construction and characterization of a chimeric fusion protein  
 associating an anti-idiotype antibody mimicking a breast cancer-  
 associated antigen and the cytokine GM-CSF";  
 RL Hybridoma 18:193-202 (1999).  
 DR EMBL; AF124721; AAK55120.1; --.

DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 1.  
 FT NON\_TER 127 127  
 SQ SEQUENCE 127 AA; 13794 MW; 13F61BBB8B981FA5 CRC64;  
  
 Alignment Scores:  
 Pred. No.: 3.69e-41 Length: 127  
 Score: 439.00 Matches: 88  
 Percent Similarity: 77.95% Conservative: 11  
 Best Local Similarity: 69.29% Mismatches: 28  
 Query Match: 62.89% Indels: 0  
 DB: 11 Gaps: 0  
  
 US-08-728-463B-206 (1-388) x Q925S9 (1-127)

QY 7 ATGATGTCCTCCGCTCAGCTCTGGGCTCTGCTGCTCTCCAGGTTCCAGATGC 66  
 Db 1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuPheProGlyThrArgCys 20  
 QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCATCTGTAGGAGACAGATCACC 126  
 Db 21 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerLeuGlyGlnArgValSer 40  
 QY 127 ATCACTTGTCTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGATCAGCATAACCA 186  
 Db 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro 60  
 QY 187 GGGAAACCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 246  
 Db 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80  
 QY 247 AGGTTTCAGCGGAGTCGATCTGGAGAGATTTCACTCTACCATCAGCAGCTGACGCT 306  
 Db 81 ArgPheSerGlySerArgSerGlySerAspThrSerLeuThrIleSerSerLeuGlnSer 100  
 QY 307 GAAGATTTTGCACTTACTATTGTCACAGCTTAATAGTTTCCGTCACATCTTTGGCCAG 366  
 Db 101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120  
 QY 367 GGGACCAAGCTGGAGATCAAA 387  
 Db 121 GlyThrLysLeuGluIleLys 127  
  
 RESULT 10  
 Q91WS9 PRELIMINARY; PRT; 233 AA.  
 AC Q91WS9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Hypothetical 25.8 kDa protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COLON;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013496; AAH13496.1; --  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;  
  
 Alignment Scores:  
 Pred. No.: 3.24e-40 Length: 233  
 Score: 431.00 Matches: 84  
 Percent Similarity: 82.05% Conservative: 12  
 Best Local Similarity: 71.79% Mismatches: 21



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RN NCBI\_TaxID=10090;  
RP [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=SPLEEN;  
RX MEDLINE=20183931; PubMed=10706631;  
RA Shinohara N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phage display subtraction  
RT method.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL; AB036341; BAB8633.1; -.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
SQ SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;

Alignment Scores:  
Pred. No.: 9e-36 Length: 298  
Score: 392.00 Matches: 74  
Percent Similarity: 81.98% Conservative: 17  
Best Local Similarity: 66.67% Mismatches: 20  
Query Match: 56.16% Indels: 0  
DB: 11 Gaps: 0

US-08-728-463B-206 (1-388) x Q9QYP0 (1-298)

QY	55	GGTTCAGATGCCACATCCAGATCCAGATCCAGATCCATCTCCGTCTCGATCTGTAGGA	114
Db	169	GlyGlyGlySerAspIleGluThrGlnSerProAlaSerLeuSerAlaSerValGly	188
QY	115	GACAGAGTCAACATCTCTGCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGTAT	174
Db	189	GluThrValThrIleThrCysArgAlaSerGlyAsnIleHisAsnIleuAlaIlePyr	208
QY	175	CAGCATAAACCCAGGAAAGCCCTAAGCTCTCTGATCTATGTCATCCAGTTTGCAAAGT	234
Db	209	GlnGlnLysGlnGlyLysSerProGlnLeuLeuValTyrAsnAlaLysThrLeuAlaAsp	228
QY	235	GGGTCCTCCATCAAGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGC	294
Db	229	GlyValProSerArgPheSerGlySerGlyThrGlnTyrSerLeuLysIleAsn	248
QY	295	AGCTGCAGCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC	354
Db	249	SerLeuGlnProGluAspPheGlySerTyrIleCysGlnHisPheThrPheThrProTyr	268
QY	355	ACTTTGGCCAGGGACCAAGCTGGAGATCAAA	387
Db	269	ThrPheGlyGlyGlyThrLysLeuGluIleLys	279

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Job time : 36.4431 secs

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Db 61 ArgPheSerGlySerGlyGlnAspTyrSerLeuThrIleSerLeuGluTyr 80
|||.....|
QY 307 GAAGATTTTGCACCTTACTATTGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCAG 366
|||.....|
Db 81 GluAspMetGlyIleTyrCysLeuGlnTyrAspGluPheProPheThrPheGlySer 100
|||.....|
QY 367 GGGACCAAGCTGGAGATCAA 387
|||.....|
Db 101 GlyThrLysLeuGluIleLys 107
|||.....|
RESULT 13
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96BEA CRC64;
Alignment Scores:
Pred. No.: 4,66e-36 Length: 108
Score: 394.00 Matches: 72
Percent Similarity: 85.98% Conservative: 20
Best Local Similarity: 67.29% Mismatches: 15
Query Match: 56.45% Indels: 0
DB: 4 Gaps: 0
US-08-728-463b-206 (1-388) x Q9UL83 (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGCATCTGTAGGACAGAGTCACC 126
|||.....|
Db 1 GluIleValMetThrGlnSerProAlaThrLeuSerValSerProGlyGluArgAlaThr 20
|||.....|
QY 127 ATCACTTGTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGTATCAGCATAAACA 186
|||.....|
Db 21 LeuSerCysArgAlaSerGlnSerValSerSerAsnLeuAlaTrpTyrGlnGlnLysPro 40
|||.....|
QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCNAAGTGGGTCCCATCA 246
|||.....|
Db 41 GlyGlnAlaProArgLeuLeuIleTyrCysAlaSerThrArgAlaThrGlyIleProAla 60
|||.....|
QY 247 AGTTTCAGCGGAGTCGGATCTGGACAGATTTTCACTCTCACCATCAGCAGCTGCAGCCT 306
|||.....|
Db 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPhe 80
|||.....|
QY 307 GAAGATTTTGCACCTTACTATTGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCAG 366
|||.....|
Db 81 GluAspPheAlaValTyrCysGlnHisTyrAsnAsnTyrProPheThrPheGlyPro 100
|||.....|
QY 367 GGGACCAAGCTGGAGATCAA 387
|||.....|

```

```

Db 101 GlyThrLysValAspIleLys 107
|||.....|
RESULT 14
Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON TER 1
FT NON TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
Alignment Scores:
Pred. No.: 6,06e-36 Length: 109
Score: 393.00 Matches: 75
Percent Similarity: 84.11% Conservative: 15
Best Local Similarity: 70.09% Mismatches: 17
Query Match: 56.30% Indels: 0
DB: 11 Gaps: 0
US-08-728-463b-206 (1-388) x Q920E6 (1-109)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGCATCTGTAGGACAGAGTCACC 126
|||.....|
Db 1 AspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerValGlyGluThrValThr 20
|||.....|
QY 127 ATCACTTGTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGTATCAGCATAAACA 186
|||.....|
Db 21 IleThrCysArgAlaSerGlyAsnIleHisAsnTyrLeuAlaTrpTyrGlnGlnLysGln 40
|||.....|
QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCNAAGTGGGTCCCATCA 246
|||.....|
Db 41 GlyLysSerProGlnLeuValTyrAsnAlaLysThrLeuAlaAspGlyValProSer 60
|||.....|
QY 247 AGTTTCAGCGGAGTCGGATCTGGACAGATTTTCACTCTCACCATCAGCAGCTGCAGCCT 306
|||.....|
Db 61 ArgPheSerGlySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnPro 80
|||.....|
QY 307 GAAGATTTTGCACCTTACTATTGTCACAGGCTAAATAGTTTCCCGTACACTTTTGCCAG 366
|||.....|
Db 81 GluAspPheGlySerTyrTyrCysGlnHisPheTyrSerThrProTyrPheGlyGly 100
|||.....|
QY 367 GGGACCAAGCTGGAGATCAA 387
|||.....|
Db 101 GlyThrLysLeuGluIleLys 107
|||.....|
RESULT 15
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CN 8 scFv.
CN 8.
OS Mus musculus (Mouse).

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: June 3, 2003, 08:56:21 ; Search time 25.0964 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-206  
Perfect score: 698  
Sequence: 1 ATGGACATGATGTCCTCCGCC.....GACCAAGCTGGAGATCAAC 388

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp  
-O=/cgn2.1/USPTO.spool/US08728463/runat\_03062003.085613.16797/app.query.fasta\_1.3690  
-DB=A\_Geneseq\_101002 -QFMT=faetan -SUFFIX=rag -MINMATCH=0.1 -LOPCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	624	89.4	236	23	AAU74297	Anti-human AILIM m
2	589.5	84.5	241	22	AA82912	Human immune respo
3	588	84.2	130	16	AA75394	Anti-interleukin-1
4	584	83.7	130	21	AA56737	Amino acid sequenc
5	578.5	82.9	237	21	AA96298	Human IGFAM-10 imm
6	575	82.4	129	19	AA70379	Anti-human CD23 SE
7	574.5	82.3	237	21	AA96289	Human IGFAM-1 immu
8	574.5	82.3	237	21	AA96301	Human IGFAM-13 imm
9	573	82.1	128	17	AAW01527	Monoclonal antibod
10	573	82.1	128	18	AAW24990	Monoclonal antibod
11	573	82.1	129	21	AA56722	Amino acid sequenc
12	571	81.8	129	23	ABG35326	Thrombopoietin ago
13	571	81.8	132	18	AAW2842	Human anti-tumour
14	571	81.8	134	23	AAW47645	Human protein sequ
15	569	81.5	260	23	ABP41164	Human ovarian anti
16	568	81.4	124	21	AA56723	Amino acid sequenc
17	568	81.4	129	16	AA65018	93KA9 anti-Varicel
18	567.5	81.3	234	14	AA38162	Sequence of the ka
19	567	81.2	234	13	AA20058	Light chain of 3p6
20	565	80.9	146	22	AA89115	Human protein SEQ
21	558	79.9	139	23	ABP43157	Human ovarian anti
22	557	79.8	129	15	AA57482	Humanized 1308F VL
23	557	79.8	129	17	AA92085	Humanized antibody
24	556	79.7	236	21	AA96297	Human IGFAM-9 immu
25	554.5	79.4	128	21	AA56717	Amino acid sequenc
26	553.5	79.3	237	21	AA815546	Human immune syste
27	553	79.2	129	21	AA56724	Amino acid sequenc
28	553	79.2	236	14	AA42065	Human anti-HBs lig
29	548	78.5	234	18	AAW11638	Human anti-RSV mon
30	545	78.1	236	21	AA96293	Human IGFAM-5 immu
31	543	77.8	133	17	AA87057	CDR grafted anti-1
32	541.5	77.6	212	22	ABG18767	Novel human diagno
33	540	77.4	129	21	AA56721	Amino acid sequenc
34	539	77.2	117	14	AA38651	Human V-kappa frag
35	539	77.2	117	15	AA62931	Human V-kappa vk65
36	539	77.2	117	17	AAW03949	DNA fragment vk65
37	539	77.2	117	18	AAW41147	Human vkappa65.15
38	539	77.2	117	19	AAW62185	Human DNA vkappa65
39	539	77.2	117	20	AA40432	Amino acid sequenc
40	539	77.2	171	17	AAW03725	Humanised MAB 39-1
41	535	76.6	236	16	AAW77614	Humanised 5G1.1 VL
42	535	76.6	236	23	ABP51696	5G1.1 light chain
43	534	76.5	128	15	AA54053	Sequence of the VL
44	532	76.2	264	19	AAW73049	Humanised A33 scAb
45	532	76.2	532	19	AAW73051	Z33CH2.z chimeric

## ALIGNMENTS

RESULT 1  
AAU74297  
ID AAU74297 standard; Protein; 236 AA.  
XX  
AC AAU74297;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.  
XX  
KW Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
KW antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;  
KW immunosuppressive; dermatologic; antiinflammatory; hepatotropic;  
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;  
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;  
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;  
KW systemic lupus erythematosus; autoimmune disorder; inflammation;  
KW graft versus host reaction; immune rejection; intestinal immunity;







KW Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;  
 KW infection; inflammation; haematopoiesis; AIDS; allergy.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 XX Peptide 1..22  
 FT /label= signal\_peptide  
 FT Protein 23..237  
 FT /label= IGFAM-10  
 FT Domain 38..112  
 FT /label= Ig\_domain  
 FT Domain 150..219  
 FT /label= Ig\_domain  
 FT Domain 193..236  
 FT /label= Ig\_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US27566.

XX 19-NOV-1998; 99US-0113635.

XX 22-DEC-1998; 98US-0113635.

XX 07-APR-1999; 99US-0128194.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
 PI Lu DM, Lal P, Hillman JL, Yang J;  
 XX

DR WPI; 2000-387796/33.

DR N-PSDB; AAA27390.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
 PT protein is useful for preventing and treating disorders associated with  
 PT altered levels of the protein such as cancer, immune system disorders  
 FT

XX Claim 1; Page 85-86; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein  
 CC IGFAM-10. Its gene was isolated from a cDNA library of colon  
 CC tissue. It is expressed in reproductive, gastrointestinal and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia,  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.  
 XX

XX Sequence 237 AA;

Alignment Scores:  
 Pred. No.: 1.69e-51 Length: 237  
 Score: 578.50 Matches: 115  
 Percent Similarity: 92.31% Conservative: 5  
 Best Local Similarity: 88.46% Mismatches: 9  
 Query Match: 82.88% Indels: 1  
 DB: 21 Gaps: 1

US-08-728-463B-206 (1-388) x AAY96298 (1-237)

QY 1 ATGCACATGATGCTCCCGCTCAGCTCCTGGGCTCTGCTGCTGCTCCAGGTTC 60  
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuThrPleuArgGlyAla 20

QY 61 AGATGGACATCCAGATGACCCAGCTCTCCATCTTCGCTGCTCTGATCTCTAGGACACAGA 120  
 Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
 QY 121 GTCCACCATCATTGTCGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCTGGTATCAGCAT 180  
 Db 41 ValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAsnTrpTyrlleuGln 60  
 QY 181 AAACACAGGAAAGCCCTAAGCTCTGATCTATGCTGTCATCCAGTTTGCAAGTGGGTC 240  
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyrlleuAlaAlaSerSerLeuGlnSerGlyVal 80  
 QY 241 CCATCAAGTTTCAGCGGAGTCGAGTGGAGAGATTTTCACTCTCACCATCAGCACCTG 300  
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrleuThrIleSerSerLeu 100  
 QY 301 CAGCCTGAAGATTTTGCACTTACTATTCTCAACAGGCTAATAGTTTC---CGTTACACT 357  
 Db 101 GlnProGluAspPheAlaThrTyrlleuGlnSerTyrlleuThrProIleThr 120  
 QY 358 TTTGGCCAGGGACCAAGCTGGAGATCAAA 387  
 Db 121 PheGlyGlnGlyThrArgLeuGluIleLys 130

RESULT 6

AAW70379

ID AAW70379 standard; Protein; 129 AA.

XX AAW70379;

XX 18-NOV-1998 (first entry)

XX Anti-human CD23 5B8 monoclonal antibody light chain variable region.  
 DE human CD23 5B8 monoclonal antibody; light chain variable region;  
 KW human CD23; IgE; FcεRI/CD23; gamma-1 constant region;  
 KW gamma-3 constant region; allergy; inflammation; autoimmune disease;  
 KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.  
 XX

OS Macaca fascicularis

XX Key Location/Qualifiers

FT Protein 1..22 /note= "signal peptide"

FT Protein 23..129 /note= "anti-human CD23 5B8 light chain variable region"

FT Binding-site 46..56 /note= "CDR 1"

FT Binding-site 72..77 /note= "CDR 2"

FT Binding-site 111..119 /note= "CDR 3"

XX WO9837099-A1.

XX 27-AUG-1998.

XX 17-FEB-1998; 98WO-US02253.

XX 05-FEB-1998; 98US-0803085.

XX 20-FEB-1997; 97US-0803085.

XX (IDEC-) IDEC PHARM CORP.

XX (SECK) SEIKAGAKU CORP.

XX Kloetzer WS, Nakamura T, Reff ME;

XX WPI; 1998-467495/40.

XX N-PSDB; AAV33309.

XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE  
 PT expression to treat or prevent allergic, inflammatory and

PT auto:immune conditions

XX Example 1; Pages 106-108; 146pp; English.

XX The present sequence represents the light chain variable region of  
 CC primate monoclonal antibody anti-human CD23 5E8. The invention  
 CC provides monoclonal antibodies which specifically bind human  
 CC CD23, the low affinity receptor for IgE (FcεRI/CD23), and comprise  
 CC either of a human gamma-1 or human gamma-3 constant region that binds  
 CC to human Fc gamma receptors and inhibits IgE expression. The monoclonal  
 CC antibodies of the invention are claimed to be useful for inhibiting  
 CC induced IgE production for treating or preventing allergic, inflammatory  
 CC and autoimmune conditions e.g. allergic rhinitis conjunctivitis,  
 CC autoimmune haemolytic anaemia, etc.

XX Sequence 129 AA;

SQ Alignment Scores:

Pred. No.: 3 45e-51 Length: 129  
 Score: 575.00 Matches: 111  
 Percent Similarity: 90.70% Conservative: 6  
 Best Local Similarity: 86.05% Mismatches: 12  
 Query Match: 82.38% Indels: 0  
 DB: 19 Gaps: 0

US-08-728-463B-206 (1-388) x AA70379 (1-129)

QY 1 ATGGACATGATGTCCTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTCCAGGTTCC 60  
 DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTyrLeuProGlyAla 20  
 QY 61 AGATGCGACATCCAGATGACCATCCATCTCCATCTCCGTCGTGCTGATCTGAGGACAGA 120  
 DB 21 ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg 40  
 QY 121 CTCACCATCTGTCGGCGGAGTCAGGATATTAGCAGCTGGTTAGCTGCTATCAGCAT 180  
 DB 41 ValThrIleThrCysArgAlaSerGlnAspIleArgTyrTyrLeuAsnIlePyrGlnGln 60  
 QY 181 AACACGGGAAGCCCTAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 240  
 DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyVal 80  
 QY 241 CCATCAAGGTTTCAGCGGAGTCGATCTGGGACAGATTTCACTCTCCATCCATCAGCAGCTG 300  
 DB 81 ProSerArgPheSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGly 100  
 QY 301 CAGCTGAAGATTTTGCACACTTACTATTGTCAACAGGCTAATAGTTTCCGTCACACTTTT 360  
 DB 101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrProArgThrPhe 120  
 QY 361 GCCCAGGGGACCAAGCTGGAGATCAA 387  
 DB 121 GlyGlnGlyThrLysValGluIleLys 129

RESULT 7

AA96289  
 ID AA96289 standard; protein; 237 AA.

XX AC AA96289;

XX DT 16-AUG-2000 (first entry)

XX DE Human IGFAM-1 immunoglobulin.

XX KW Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;  
 XX KW infection; inflammation; haematopoiesis; AIDS; allergy.

XX OS Homo sapiens.

XX FH . Key Location/Qualifiers  
 XX FT Peptide 1..22  
 XX FT /label= signal\_peptide

FT Protein 23..237  
 FT /label= IGFAM-1  
 FT Domain 38..112  
 FT /label= Ig\_domain  
 FT Domain 150..219  
 FT /label= Ig\_domain  
 FT Region 154..176  
 FT /label= Ig\_signature  
 FT Domain 193..236  
 FT /label= Ig\_domain  
 FT Region 215..232  
 FT /label= Ig\_signature

PN W0200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US27566.

XX 19-NOV-1998; 99US-0113635.

XX 22-DEC-1998; 98US-0113635.

XX 07-APR-1999; 99US-0128194.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;

PI Lu DAM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27381.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
 PT protein is useful for preventing and treating disorders associated with  
 PT altered levels of the protein such as cancer, immune system disorders

XX Claim 1; Page 77-78; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein  
 CC IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane  
 CC tissue. It is expressed in reproductive, gastrointestinal and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.

XX SQ Sequence 237 AA;

Alignment Scores:

Pred. No.: 4 38e-51 Length: 237  
 Score: 574.50 Matches: 114  
 Percent Similarity: 91.54% Conservative: 5  
 Best Local Similarity: 87.69% Mismatches: 10  
 Query Match: 82.31% Indels: 1  
 DB: 21 Gaps: 1

US-08-728-463B-206 (1-388) x AA96289 (1-237)

QY 1 ATGGACATGATGTCCTCCCGCTCAGCTCTGGGGCTCTGCTGCTCTGCTCCAGGTTCC 60

DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTyrLeuProGlyAla 20

QY 61 AGATGCGACATCCAGATGACCATCCATCTCCATCTCCGTCGTGCTGATCTGAGGACAGA 120

DB 21 ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg 40



QY 121 GTCACATCACTGTCTGGCGAGTCAGGATATTAGCAGCTGCTAGCCTGGTATCAGCAT 180  
 Db 41 ValThrIleThrCysArgAlaGlyGlnSerIleSerSerTyRLeuAsnTrpTyRLeuGln 60  
 QY 181 AAACACAGGGAAGCCCTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAAGTGGGTC 240  
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyRAlaAlaSerSerLeuGlnSerGlyVal 80  
 QY 241 CCATCAGGTTACGGCGAGTCGATCTGGACAGATTTCACCTCACCATCAGCAGCCTG 300  
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
 QY 301 CAGCCTGAAGATTTCACCTACTATTCTCAACAGGCTAATAGTTTC---CCGTACACT 357  
 Db 101 GlnProGluAspPheAlaThrTyRtyrCysGlnGlnSerTyRThrProIleThr 120  
 QY 358 TTGGCCAGGGACCAAGCTGGAGATCAAA 387  
 Db 121 PheGlyGlnGlyThrArgLeuGluIleLys 130  
 RESULT 8  
 AAY96301  
 ID AAY96301 standard; protein; 237 AA.  
 AC AAY96301;  
 XX  
 XX  
 DT 16-AUG-2000 (first entry)  
 XX  
 DE Human IGFAM-13 immunoglobulin.  
 XX  
 KW Human; immunoglobulin, IGFAM-13; IGFAM; immune disorder; cancer;  
 KW infection; inflammation; haematopoiesis; AIDS; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..22 Location/Qualifiers  
 FT /label= signal\_peptide  
 FT Protein 23..237  
 FT /label= IGFAM-13  
 FT Domain 38..112  
 FT /label= Ig\_domain  
 FT Domain 150..219  
 FT /label= Ig\_domain  
 FT Domain 193..236  
 FT /label= Ig\_domain  
 XX  
 PN WO200029583-A2.  
 XX  
 XX 25-MAY-2000.  
 PD  
 PF 19-NOV-1999; 99WO-US27566.  
 XX  
 XX 19-NOV-1998; 99US-0113635.  
 PR 22-DEC-1998; 98US-0113635.  
 PR 07-APR-1999; 99US-0128194.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
 PI Lu DAN, Lal P, Hillman JL, Yang J;  
 PI  
 XX WPI; 2000-387796/33.  
 DR N-PSDB; AAA27393.  
 XX  
 XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
 PT protein is useful for preventing and treating disorders associated with  
 PT altered levels of the protein such as cancer, immune system disorders  
 PT  
 XX  
 XX Claim 1; Page 87-88; 105pp; English.  
 PS  
 XX The present sequence is the human immunoglobulin superfamily protein  
 CC

CC IGFAM-13. Its gene was isolated from a cDNA library of lung tumour  
 CC tissue. It is expressed in reproductive, gastrointestinal and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia,  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.  
 XX Sequence 237 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 4,38e-51 Length: 237  
 Score: 574.50 Matches: 112  
 Percent Similarity: 93.08% Conservative: 9  
 Best Local Similarity: 86.15% Mismatches: 8  
 Query Match: 82.31% Indels: 1  
 DB: 21 Gaps: 1  
 US-08-728-463B-206 (1-388) x AAY96301 (1-237)  
 QY 1 ATGGAATGATGCTCCCGCTCAGCTCTGGGGCTCTGCTCTGTTCCAGTTCC 60  
 Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20  
 QY 61 AGATCGGACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGCATCTCTAGGAGACAGA 120  
 Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
 QY 121 GTCACATCACTTGTCTGGCGAGTCAGGATATTAGCAGCTGTTAGCCTGGTATCAGCAT 180  
 Db 41 ValThrMetThrCysArgAlaSerGlnSerIleSerThrTyRLeuAsnTrpTyRLeuGln 60  
 QY 181 AAACACAGGGAAGCCCTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAAGTGGGTC 240  
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyRAlaAlaSerSerLeuGlnSerGlyVal 80  
 QY 241 CCATCAGGTTACGGCGAGTCGATCTGGACAGATTTCACCTCACCATCAGCAGCCTG 300  
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
 QY 301 CAGCCTGAAGATTTCACCTACTATTCTCAACAGGCT---AATAGTTTCCGTACACT 357  
 Db 101 GlnProGluAspPheAlaThrTyRtyrCysGlnGlnSerPheAsnThrHisMetTyRThr 120  
 QY 358 TTGGCCAGGGACCAAGCTGGAGATCAAA 387  
 Db 121 PheGlyGlnGlyThrArgLeuGluMetLys 130  
 RESULT 9  
 AAW01527  
 ID AAW01527 standard; Protein; 128 AA.  
 XX  
 XX AAW01527;  
 AC  
 XX 04-MAR-1997 (first entry)  
 DT  
 XX Monoclonal antibody ZM1-2 light chain variable region.  
 DE  
 XX Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;  
 KW xenogeneic hybridoma; SPAZ 4; PEI-1; ZM1-1; ZM1-2; MD3-4; L03-3;  
 KW IgG1 class; heavy chain; light chain; variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..20 Location/Qualifiers  
 FT /label= leader\_sequence  
 FT







```
CC human MAB CLN"-Igm identified by western blotting.
XX
SQ Sequence 132 AA;

Alignment Scores:
Pred. No.: 9e-51 Length: 132
Score: 571.00 Matches: 112
Percent Similarity: 90.70% Conservative: 5
Best Local Similarity: 86.82% Mismatches: 12
Query Match: 81.81% Indels: 0
DB: 18 Gaps: 0

US-08-728-463B-206 (1-388) x AAW22842 (1-132)
QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTGCTGGGCTCTGCTGCTGGTCCAGGTTCC 60
DB 1 MetAspMetGluAlaHisValGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20
QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTCCGCTGCTGCATCTGTAGGAGACAGA 120
DB 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCACCATCATTGTCCGGCGAGTCAAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCAT 180
DB 41 ValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrlleuAsnTrpTyrlleuGln 60
QY 181 AAACAGGAGAAAGCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC 240
DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrlleuAlaSerSerLeuGlnSerGlyVal 80
QY 241 CCATCAAGCTTCAGCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
DB 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTTT 360
DB 101 GlnProGluAspPheAlaThrTyrlleuTyrlleuGlnSerTyrlleuProGlnThrPhe 120
QY 361 GGCCAGGGACCAAGCTGGAGATCAAA 387
DB 121 GlyGlnGlyThrLysValGluIleLys 129

RESULT 14
AAW47645
ID AAW47645 standard; Protein; 134 AA.
AC AAW47645;
XX
DT 15-FEB-2002 (first entry)
DE Human protein sequence #3.
XX
KW Human; cytostatic; antiinflammatory; antianaemic; vasotropic;
KW antibody; signal transmission; cancer; inflammation; hormonal disorder;
KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
XX
OS Homo sapiens.
XX
PN WO200179494-A1.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-JP03288.
XX
PR 17-APR-2000; 2000JP-0115246.
PR 20-OCT-2000; 2000JP-0321821.
PR 20-OCT-2000; 2000JP-0321822.
PR 12-MAR-2001; 2001WO-JP01912.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;
XX

DR WPI: 2002-066368/09.
XX N-PSDB; ABA04572.
PT Antibodies for treatment of diseases associated with cell
PT proliferation, hormonal disorders and cytokines comprise agonist
PT activity to signal transmission across cell membranes -
XX
PS Disclosure; Page 164; 173pp; Japanese.
XX
CC The present invention relates to modified antibodies. The antibodies
CC contain two or more H chain V domains and two or more L chain V domains
CC of a monoclonal antibody (Mab) which is capable of transmitting a signal
CC across the cell membrane by cross-linking a cell surface molecule, where
CC the antibodies can serve as signal transmission agonists. The antibodies
CC are useful for treatment and prevention of a broad range of disorders in
CC which signal transmission is implicated, such as cancer, inflammation,
CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
CC skeletal malformations. The present sequence was used to illustrate the
CC present invention.
XX
SQ Sequence 134 AA;

Alignment Scores:
Pred. No.: 9.03e-51 Length: 134
Score: 571.00 Matches: 107
Percent Similarity: 90.70% Conservative: 10
Best Local Similarity: 82.95% Mismatches: 12
Query Match: 81.81% Indels: 0
DB: 23 Gaps: 0

US-08-728-463B-206 (1-388) x AAW47645 (1-134)
QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTGCTGGGCTCTGCTGCTGGTCCAGGTTCC 60
DB 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAla 20
QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTCCGCTGCTGCATCTGTAGGAGACAGA 120
DB 21 LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerIleGlyAspArg 40
QY 121 GTCACCATCATTGTCCGGCGAGTCAAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCAT 180
DB 41 ValThrIleThrCysArgAlaSerGluGlyIleTyrlleuThrleuAlaTrpTyrlleuGln 60
QY 181 AAACAGGAGAAAGCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC 240
DB 61 LysProGlyLysAlaProLysLeuLeuIleTyrlleuAlaSerSerLeuGlnSerGlyAla 80
QY 241 CCATCAAGCTTCAGCGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTG 300
DB 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
QY 301 CAGCCTGAAGATTTGCAACTTACTATTGTCAACAGGCTAAATAGTTTCCCGTACACTTTT 360
DB 101 GlnProGluAspPheAlaThrTyrlleuTyrlleuGlnSerTyrlleuProGlnThrPhe 120
QY 361 GGCCAGGGACCAAGCTGGAGATCAAA 387
DB 121 GlyGlyGlyThrLysLeuGluIleLys 129

RESULT 15
ABP41164
ID ABP41164 standard; Protein; 260 AA.
XX
AC ABP41164;
XX
DT 23-AUG-2002 (first entry)
XX
DE Human ovarian antigen HRACW30, SEQ ID NO:2296.
XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX
```

KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive; chromosome 2p12.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WPI; 2002-147878/19.  
 DR N-PSDB; ABQ54241.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX

Claim 11; SEQ ID No 2296; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ563305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 260 AA;

Alignment Scores:			
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US-08-728-463B-206 (1-388) x ABP41164 (1-260)

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Db	25	MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla	44
Qy	61	AGATGGACATCCAGATGACCCAGTCTCCATCTCCGTCGTCATCTCTAGAGACAGA	120
Db	45	ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg	64
Qy	121	GTCAACATCACTTGTCTGGCGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCAT	180
Db	65	ValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrIleAsnTrpIleGlnGln	84
Qy	181	AAACAGGGAAGCCCTTAAGCTCTGATCTATGTGTCATCCAGTTTGCAAGTGGGGTC	240
Db	85	LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSer**LeuGlnSerGlyVal	104
Qy	241	CCATCAAGGTTTCCAGCGGCGAGTCGATCTGGGACAGATTTTCACTCTCCATCAGCAGCCTG	300
Db	105	ProSerArgPheSerGlySerGlyThrAspPheThr**ThrIleSerSerLeu	124
Qy	301	CAGCTGAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTT	360
Db	125	GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAspAsn**ProLeuThrPhe	144
Qy	361	GGCAGGAGGACCAAGCTGGAGATCAA 387	
Db	145	Gly**GlyThrLysValGluIleLys 153	

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Job time : 28.263 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 16.4856 Seconds

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Title: US-08-728-463B-206

Perfect score: 698

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Total number of hits satisfying chosen parameters: 767038

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	548	78.5	234	10	US-09-740-002-24
3	543	77.8	128	10	US-09-855-271-26
4	535	76.6	236	9	US-10-006-593-69

Sequence 30, Appl

Sequence 24, Appl

Sequence 26, Appl

Sequence 69, Appl

Sequence 26, Appl

Sequence 4, Appl

Sequence 1881, Ap

Sequence 88, Appl

Sequence 10, Appl

Sequence 5, Appl

Sequence 12, Appl

Sequence 6, Appl

Sequence 92, Appl

Sequence 2, Appl

Sequence 12, Appl

Sequence 2, Appl

Sequence 17, Appl

Sequence 40, Appl

Sequence 8, Appl

Sequence 150, App

Sequence 152, App

Sequence 7, Appl

Sequence 1906, Ap

Sequence 2003, Ap

Sequence 2005, Ap

Sequence 2017, Ap

Sequence 2019, Ap

Sequence 2020, Ap

Sequence 2027, Ap

Sequence 2028, Ap

Sequence 2040, Ap

Sequence 2043, Ap

Sequence 2104, Ap

Sequence 1580, Ap

Sequence 1291, Ap

Sequence 1004, Ap

Sequence 1385, Ap

Sequence 1717, Ap

Sequence 1719, Ap

Sequence 1733, Ap

#### ALIGNMENTS

RESULT 1

US-09-859-053-30

; Sequence 30, Application US/09859053

; Patent No. US20020102658A1

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Hori, No. US20020102658A1uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; FILE REFERENCE: 06501-079001

; CURRENT APPLICATION NUMBER: US/09/859,053

; PRIOR FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: JP 2000-147116

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-859-053-30

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Pred. No.: 3.2e-46 Length: 236

Db 1 MetGluThrProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCys 20  
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 Db 21 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 40  
 QY 127 ATCACTTTGTCGGCGAGTCCAGATATTACGACCTGGTTAGCCTGGTATCAGCATAAACCA 186  
 Db 41 IleThrCysArgAlaGlyGlnArgIleAlaSerTyrLeuAsnTrpTyrGlnHisLysPro 60  
 QY 187 GGGAAAGCCCTAAAGTCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTGCCCATCA 246  
 Db 61 GlyLysAlaProLysLeuLeuIleTyrAlaGlySerAsnLeuHisArgGlyValProSer 80  
 QY 247 AGTTTCAGCGGAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGCCTGCAGCCT 306  
 Db 81 ArgPheSerGlyGlyGlySerGlyThrAspPheThrLeuThrIleAsnSerLeuGlnPro 100  
 QY 307 GAAGATTTTGGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
 Db 101 GluAspPheAlaThrTyrTyrCysGlnAlaTyrSerThrProTrpThrPheGlyPro 120  
 QY 367 GGGACCAAGCTGGAGATCAAA 387  
 Db 121 GlyThrLysValGluIleLys 127  
 RESULT 3  
 US-09-855-271-26  
 ; Sequence 26, Application US/09855271  
 ; Patent No. US20020042089A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bodmer, Mark W  
 ; APPLICANT: Athwal, Diljeet Singh  
 ; APPLICANT: Emage, John Spencer  
 ; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies  
 ; FILE REFERENCE: CARP-0088  
 ; CURRENT APPLICATION NUMBER: US/09/855,271  
 ; CURRENT FILING DATE: 2001-05-15  
 ; PRIOR APPLICATION NUMBER: 09/347,061  
 ; PRIOR FILING DATE: 1999-07-02  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 128  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: No. US20020042089A1el Sequence  
 US-09-855-271-26  
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 Pred. No.: 3,34e-39 Length: 128  
 Score: 543.00 Matches: 103  
 Percent Similarity: 89.76% Conservative: 11  
 Best Local Similarity: 81.10% Mismatches: 13  
 Query Match: 77.79% Indels: 0  
 DB: 10 Gaps: 0  
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 QY 7 ATGATGGTCCCCGCTCAGCTCTGGGGCTCTCTGCTGCTGGTCCAGGTTCCAGATGC 66  
 Db 1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrAspAlaArgCys 20  
 QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGCATCTGTAGGACACAGAGTCACC 126  
 Db 21 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 40  
 QY 127 ATCACTTTGTCGGCGAGTCCAGATATTACGACCTGGTTAGCCTGGTATCAGCATAAACCA 186  
 Db 41 IleThrCysLeuAlaSerGluGlyIleSerSerTyrLeuAlaTrpTyrGlnLysPro 60  
 QY 187 GGGAAAGCCCTTAAGCTCTGATCTATGTCATCCAGTTTTCGAAAGTGGGTGCCCATCA 246



Db 61 GlyLysAlaProLysLeuLeuIleTyrGlyAlaAsnSerLeuGlnThrGlyValProSer 80  
QY 247 AGTTTCAGCGGAGTGGTCTGGACAGATTTTCACTCTCCACCATCAGCAGCCTGCAGCCT 306  
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyrThrLeuThrIleSerSerLeuGlnPro 100  
QY 307 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366  
Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnThrPheGlyGln 120  
QY 367 GGGACCAAGCTGGAGATCAAA 387  
Db 121 GlyThrLysValGluValLys 127

## RESULT 4

US-10-006-593-69  
; Sequence 69, Application US/10006593  
; Publication No. US20030049683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2  
; CURRENT APPLICATION NUMBER: US/10/006,593  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/288,889  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,068  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody light chain  
US-10-006-593-69

Alignment Scores:  
Pred. No.: 1,58e-38 Length: 236  
Score: 535.00 Matches: 104  
Percent Similarity: 86.82% Conservative: 8  
Best Local Similarity: 80.62% Mismatches: 17  
Query Match: 76.65% Indels: 0  
DB: 9 Gaps: 0

US-08-728-463B-206 (1-388) x US-10-006-593-69 (1-236)

QY 1 ATGGACATGATGCTCCCGCTAGCTCTGGGGCTCTCTGCTGCTGTTCCAGGTTCC 60  
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla 20  
QY 61 AGATGGACATCAGATGACCCAGTCTCCATCTTCGGTGTCTGCTATCTGTAGGAGACAGA 120  
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
QY 121 GTACCATCATCTTGTCTGGGGAGTCAAGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180  
Db 41 ValThrIleThrCysArgAlaSerGlnSerIleAlaSerTyrValAsnTrpTyrGlnGln 60  
QY 181 AAACACGGGAAGCCCTAGCTCTGATCTATGCTGTCATCCAGTTTGCAGTGGGCTC 240  
Db 61 LysProGlyLysAlaProLysLeuLeuIleTyrGlyAlaThrAsnLeuAlaAspGlyVal 80  
QY 241 CCATCAAGTTTACGCGGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG 300  
Db 81 ProSerArgPheSerGlySerGlyThrValPheThrLeuThrIleSerSerLeu 100

QY 301 CAGCTTGAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCGTACACTTTT 360  
Db 101 GlnProGluAspPheAlaThrTyrTyrCysGlnAsnValLeuAsnThrProLeuThrPhe 120  
QY 361 GCCCAGGGAGCAACGCTGGAGATCAAA 387  
Db 121 GlyGlnGlyThrLysValGluIleLys 129

## RESULT 5

US-09-740-002-26  
; Sequence 26, Application US/09740002  
; Patent No. US20020001798A1  
; GENERAL INFORMATION:  
; APPLICANT: MORROW, PHILLIP

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES  
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR  
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0275759

; CURRENT APPLICATION NUMBER: US/09/740,002  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/335,697  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 08/488,376  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-002-26

## Alignment Scores:

Pred. No.: 8.6e-38 Length: 234  
Score: 526.50 Matches: 102  
Percent Similarity: 91.47% Conservative: 16  
Best Local Similarity: 79.07% Mismatches: 10  
Query Match: 75.43% Indels: 1  
DB: 10 Gaps: 1

US-08-728-463B-206 (1-388) x US-09-740-002-26 (1-234)

QY 1 ATGGACATGATGCTCCCGCTAGCTCTGGGGCTCTCTGCTGCTGTTCCAGGTTCC 60  
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla 20  
QY 61 AGATGGACATCAGATGACCCAGTCTCCATCTTCGGTGTCTGCTATCTGTAGGAGACAGA 120  
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
QY 121 GTACCATCATCTTGTCTGGGGAGTCAAGATATTAGCAGCTGGTTAGCCTGGTATCAGCAT 180  
Db 41 ValThrIleThrCysArgAlaSerGlnSerIleAlaSerTyrValAsnTrpTyrGlnGln 60  
QY 181 AAACACGGGAAGCCCTAGCTCTGATCTATGCTGTCATCCAGTTTGCAGTGGGCTC 240  
Db 61 LysProGlyLysAlaProLysValLeuIlePheAlaSerAlaAsnLeuValSerGlyVal 80  
QY 241 CCATCAAGTTTACGCGGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG 300  
Db 81 ProSerArgPheSerGlySerGlyThrValPheThrLeuThrIleSerAsnLeu 100  
QY 301 CAGCTTGAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCGTACACTTTT 360  
Db 101 GlnProGluAspPheAlaThrTyrPheCysGlnGlnSerTyrThr---AsnPheSerPhe 119  
QY 361 GCCCAGGGAGCAACGCTGGAGATCAAA 387  
Db 120 GlyGlnGlyThrLysLeuGluIleLys 128

## RESULT 6

US-10-283-349-71

```

; Sequence 71, Application US/10283349
; Publication No. US20030096977A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, NO. US20030096977A1uo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/283,349  
FILING DATE: 29-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE 212-790-9090

TELEPHONE: 212-869-9741  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 71:

JS-10-283-349-71

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Alignment Scores:	1.47e-37	Length:	127
Aligned. No.:	524.00	Matches:	103
Percent Score:	85.03%	Conservative:	6
Percent Similarity:	81.10%	Mismatches:	18
Best Local Similarity:	75.07%	Indels:	0
Query Match:	9	Gaps:	0
DB:			

US-08-728-463B-206 (1-388) x US-10-283-349-71 (1-127)

[illegible]

QY	187	GGGAAGCCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAGATGGGGTCCCCATCA	246
Db			
Db	61	GlyLeuAlaProIysLeuLeuIleTyrHisThrSerArgLeuGlnSerGlyValProSer	80
QY	247	AGGTCAGCGGAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGCCTGACGCT	306
Db			
Db	81	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerLeuGlnPro	100
QY	307	GAAGATTTTGCACCTACTATTGTGCAACAGGCTAATAGTTTCCGTACACTTTTGCCAG	366
Db			
Db	101	GluaspPheAlaThrTyrTyrCysGlnGlnGlyTyrThrLeuProTyrThrPheGlyGln	120
QY	367	GGGACCAAGCTGGAGATCAAA	387
Db			
Db	121	GlyThrLysValGluIleLys	127

## RESULT 7

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US-09-798-058-4
; Sequence 4, Application US/09798058
; Patent No. US20020098523A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Wilton, Alison Jane
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against ectaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-4

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Alignment Scores:	2.43e-37	Length:	109
Pred. No.:	521.50	Matches:	103
Score:	97.22%	Conservative:	2
Percent Similarity:	95.37%	Mismatches:	2
Best Local Similarity:	74.71%	Indels:	1
Query Match:	10	Gaps:	1
DB:			

US-08-728-463B-206 (1-388) x US-09-798-058-4 (1-109)

[illegible]

US-10-283-349-88  
; Sequence 88, Application US/10283349  
; Publication No. US20030096977A1  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masaamichi  
; FURUYA, Akiko  
; NAGAWARA, Kazuyasu  
; IIDA, Akihiro  
; ANAZAWA, Hideharu  
; HANAI, No. US20030096977A1uo

Qy	7	ATGATGTGTC	CGCGT	CTAGCT	CCTGGGG	CTCTGCT	GTCTGCT	GTGTTCC	CAGGTTCC	AGATGC	66
Db	1	MetMetSer	AlaGln	PheLeu	GlyLeuLeuLeu	CysPhe	GlnAsp	ileArg	Cys	20	
Qy	67	GACATCCAG	ATGACC	CAGTCT	CCATCT	TCCTG	CTGCTG	CATCTG	TAGGAG	CACAGATGCAC	126
Db	21	AspIleGln	MetThr	GlnSer	ProSer	SerLeu	SerAla	SerVal	GlyAsp	argValThr	40
Qy	127	ATCACTTGT	CGCGCAG	TTCAGG	ATATTAG	CAGCTG	TGTTAG	CGCTG	TATCAG	CATAAACCA	186
Db	41	IleThrCys	GlyThr	SerGlu	AspIle	ileAsn	TyrLeu	AsnTrp	TyrArg	GlnLysPro	60
Qy	187	GGGAAAGC	CCCTA	AGCTCT	GTGATCT	ATGCTG	CTCCAT	CCAGTTG	CAAGTGG	GGTCCCATCA	246
Db	61	GlyLysAla	ProGlu	LeuLeu	IleTyr	HisThr	SerArg	GlnSer	GlyVal	ProSer	80
Qy	247	AGGTTACG	CGCGCAG	TGTGAT	CTGGG	CAGATTC	ACTCTC	ACCAT	CAGCAG	CGCTGCAGCT	306
Db	81	ArgPheSer	GlySer	GlyThr	AspPhe	ThrLeu	ThrIle	SerSer	LeuGln	Pro	100



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Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
      |||||||
QY      367 GGGACCAAGCTGGAGATCAAA 387
      |||||||
Db      101 GlyThrLysValGluIleLys 107
      |||||||

RESULT 12
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-12

Alignment Scores:
Pred. No.: 7,938-36 Length: 108
Score: 504.00 Matches: 97
Percent Similarity: 96.26% Conservative: 6
Best Local Similarity: 90.65% Mismatches: 4
Query Match: 72.21% Indels: 0
DB: 10 Gaps: 0

US-08-728-463B-206 (1-388) x US-09-056-160B-12 (1-108)

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
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Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGCGAGTCAGGATATTAGCAGCTGGTGGTATGAGCTGATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGluSerGlyValProSer 60
      |||||||

US-08-728-463B-206 (1-388) x US-09-056-160B-12 (1-108)

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
      |||||||
Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGCGAGTCAGGATATTAGCAGCTGGTGGTATGAGCTGATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGluSerGlyValProSer 60
      |||||||
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QY      247 AGGTTACGGCGAGTGGATCTGGGACAGATTTTCACTTCACCATCAGCAGCCTGCAGCCT 306
      |||||||
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
      |||||||

QY      307 GAAGATTTTGCACCTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
      |||||||
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
      |||||||

QY      367 GGGACCAAGCTGGAGATCAAA 387
      |||||||
Db      101 GlyThrLysValGluIleLys 107
      |||||||

RESULT 13
US-09-811-123-6
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB
; FILE REFERENCE: ANTIBODY-MAVTANSINOID CONJUGATES
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6

Alignment Scores:
Pred. No.: 7,928-36 Length: 109
Score: 504.00 Matches: 97
Percent Similarity: 96.26% Conservative: 6
Best Local Similarity: 90.65% Mismatches: 4
Query Match: 72.21% Indels: 0
DB: 10 Gaps: 0

US-08-728-463B-206 (1-388) x US-09-811-123-6 (1-109)

QY      67 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGTCATCTGTAGGACAGAGTCACC 126
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Db      1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
      |||||||

QY      127 ATCACTTGTGGGCGAGTCAGGATATTAGCAGCTGGTGGTATGAGCTGATCAGCATAAACCA 186
      |||||||
Db      21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
      |||||||

QY      187 GGGAAAGCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCA 246
      |||||||
Db      41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGluSerGlyValProSer 60
      |||||||

QY      247 AGGTTACGGCGAGTGGATCTGGGACAGATTTTCACTTCACCATCAGCAGCCTGCAGCCT 306
      |||||||
Db      61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
      |||||||

QY      307 GAAGATTTTGCACCTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366
      |||||||
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerLeuProtrpThrPheGlyGln 100
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QY      367 GGGACCAAGCTGGAGATCAAA 387
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Db      101 GlyThrLysValGluIleLys 107
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 QY 295 AGCTGCACGCTGAAGATTTTCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTAC 354  
 Db 209 SerLeuGlnProGluAspPheAlaThrTyTyTyCysGlnGlnSerTySerThrProAsn 228  
 QY 355 ACTTTTGGCCAGGGACCAAGCTGGAGATCAAA 387  
 Db 229 ThrPheGlyGlnGlyThrLysValGluIleLys 239

Search completed: June 3, 2003, 09:51:15  
 Job time : 18.4856 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 8.83156 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

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Perfect score: 698  
Sequence: 1 ATGGACATGATGTCCTCCGC.....GACCAAGCTGGAGATCAAC 388

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	82.1	128	1	US-08-259-372A-14
2	573	82.1	128	1	US-08-468-671-14
3	573	82.1	129	1	US-08-217-918-2
4	553	79.2	236	1	US-08-157-101A-5
5	543	77.8	128	2	US-08-470-139-26
6	543	77.8	128	4	US-09-347-061-26
7	539	77.2	117	4	US-09-042-353-48
8	539	77.2	117	4	US-08-758-417A-313
9	532	76.2	116	1	US-08-053-131-185
10	532	76.2	116	2	US-08-096-762-185
11	529	75.8	128	4	US-08-569-147-80
12	526	75.4	127	2	US-08-621-751A-6

13	524	75.1	127	3	US-08-836-561-71	Sequence 71, Appl
14	517	74.1	109	2	US-07-934-373C-3	Sequence 3, Appl1
15	517	74.1	109	3	US-08-437-642B-3	Sequence 3, Appl1
16	517	74.1	109	4	US-08-146-206C-3	Sequence 3, Appl1
17	517	74.1	109	5	PCT-US93-07832-3	Sequence 3, Appl1
18	517	74.1	127	4	US-09-136-315-8	Sequence 8, Appl1
19	513	73.5	131	4	US-08-579-378A-18	Sequence 18, Appl
20	512	73.4	128	4	US-08-569-147-78	Sequence 18, Appl
21	509	72.9	127	3	US-08-836-561-88	Sequence 88, Appl
22	509	72.9	235	3	US-08-812-586-16	Sequence 16, Appl
23	507	72.6	233	3	US-08-812-586-45	Sequence 45, Appl
24	506	72.5	127	2	US-08-621-751A-2	Sequence 2, Appl1
25	504	72.2	107	2	US-07-934-373C-18	Sequence 18, Appl
26	504	72.2	107	3	US-08-437-642B-18	Sequence 18, Appl
27	504	72.2	107	4	US-08-146-206C-18	Sequence 18, Appl
28	504	72.2	107	5	PCT-US93-07832-18	Sequence 18, Appl
29	504	72.2	108	3	US-08-974-899-3	Sequence 3, Appl1
30	504	72.2	127	3	US-08-649-100-33	Sequence 33, Appl
31	503	72.1	133	1	US-08-461-284-2	Sequence 2, Appl1
32	503	72.1	133	1	US-08-462-939-2	Sequence 2, Appl1
33	503	72.1	133	1	US-08-253-877C-2	Sequence 2, Appl1
34	503	72.1	133	2	US-08-452-164A-2	Sequence 2, Appl1
35	498	71.3	127	3	US-08-836-561-92	Sequence 92, Appl
36	495	70.9	109	4	US-09-157-370-3	Sequence 3, Appl1
37	495	70.9	127	2	US-08-646-981-8	Sequence 8, Appl1
38	495	70.9	134	4	US-08-718-323A-10	Sequence 10, Appl
39	495	70.9	134	4	US-09-587-526-10	Sequence 10, Appl
40	494.5	70.8	133	1	US-08-253-877C-28	Sequence 28, Appl
41	494.5	70.8	133	2	US-08-452-164A-28	Sequence 28, Appl
42	494.5	70.8	133	3	US-08-603-024-27	Sequence 27, Appl
43	493	70.6	128	4	US-09-450-520A-6	Sequence 6, Appl1
44	492	70.5	107	4	US-09-240-274-40	Sequence 40, Appl
45	492	70.5	138	4	US-08-976-183A-46	Sequence 46, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-259-372A-14  
; Sequence 14, Application US/08259372A  
; Patent No. 5565354  
; GENERAL INFORMATION:  
; APPLICANT: Ostberg, Lars G.  
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/259,372A  
; FILING DATE: 14-JUN-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/871,426  
; FILING DATE: 21-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/676,036  
; FILING DATE: 27-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/538,796  
; FILING DATE: 15-JUN-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/192,754



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QY 259 ACTGGATCTGGGACAGATTTCCTCTCACATCAGCAGCCTCGAGCTCAAGATTTCGA 318
Db 85 SerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAlaGluAspPheAla 104
QY 319 ACTTACTATTGTCAACAGAGCTAATAGTTCCTCCGTACACTTTTGGCCAGGGGACCAAGCTG 378
Db 105 ThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyThrIysVal 124
QY 379 GAGATCAAA 387
Db 125 AspPheLys 127

RESULT 3
US-08-217-918-2
; Sequence 2, Application US/08217918
; Patent No. 5506132
; GENERAL INFORMATION:
; APPLICANT: LAKE, PHILIP
; APPLICANT: OSTBERG, LARS
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,918
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-918-2

Alignment Scores:
Pred. No.: 4,06e-55 Length: 129
Score: 573.00 Matches: 107
Percent Similarity: 92.25% Conservative: 12
Best Local Similarity: 82.95% Mismatches: 10
Query Match: 82.09% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x US-08-217-918-2 (1-129)
QY 1 ATGGACATGATGTCCTCCGCTCAGCTCTCTGGGCTCTGCTGTGTTCCAGTTCC 60
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAla 20
QY 61 AGATGGACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGTCATCTGTAGGACAGA 120
Db 21 LysCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArg 40
QY 121 GTCACCATCATTGTCTGGGCGAGTCAAGATATTAGCAGCTGGTACCTGGTATCAGCAT 180
Db 41 ValThrIleThrCysArgAlaSerGlnThrIleSerThrTrpLeuAlaTrpTyrGlnGln 60
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QY 181 AAACAGAGGAAGCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTC 240
Db 61 ThrProArgLysAlaProLysLeuMetIleTyrLysAlaSerIleLeuGluAsnGlyVal 80
QY 241 CCATCAAGGTTTCAGGGGAGTGGATCTGGGACAGATTTTCACTCTCACCATCAGCAGCTG 300
Db 81 ProSerArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerLeu 100
QY 301 CAGCCTGAAGATTTTGCACCTTACTATTCTCAACAGGCTAATAGTTTCCCGTACATTTT 360
Db 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrLysSerTyrProIleThrPhe 120
QY 361 GCCCAGGGGACCAAGCTGGAGATCAAA 387
Db 121 GlyGlnGlyThrLysValGluIleLys 129

RESULT 4
US-08-157-101A-5
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSUROOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-5

Alignment Scores:
Pred. No.: 7,56e-53 Length: 236
Score: 553.00 Matches: 104
Percent Similarity: 89.92% Conservative: 12
Best Local Similarity: 80.62% Mismatches: 13
Query Match: 79.23% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-206 (1-388) x US-08-157-101A-5 (1-236)
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P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :   U S   0 8 / 7 2 8 , 4 6 3
F I L I N G   D A T E :   1 0 - O C T - 1 9 9 6
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :   W O   P C T / U S 9 6 / 1 6 4 3 3
F I L I N G   D A T E :   1 0 - O C T - 1 9 9 6
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :   U S   0 8 / 7 5 8 , 4 1 7
F I L I N G   D A T E :   0 2 - D E C - 1 9 9 6
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :   W O   P C T / U S 9 7 / 2 1 8 0 3
F I L I N G   D A T E :   0 1 - D E C - 1 9 9 7
A T T O R N E Y / A G E N T   I N F O R M A T I O N :
N A M E :   A p p l e ,   R a n d o l p h   T .
R E G I S T R A T I O N   N U M B E R :   3 6 , 4 2 9
R E F E R E N C E / D O C K E T   N U M B E R :   0 1 4 6 4 3 - 0 0 9 0 4 0 U S
T E L E C O M M U N I C A T I O N   I N F O R M A T I O N :
T E L E P H O N E :   ( 4 1 5 )   5 7 6 - 0 2 0 0
T E L E F A X :   ( 4 1 5 )   5 7 6 - 0 3 0 0
I N F O R M A T I O N   F O R   S E Q   I D   N O :   4 8 :
S E Q U E N C E   C H A R A C T E R I S T I C S :
L E N G T H :   1 1 7   a m i n o   a c i d s
T Y P E :   a m i n o   a c i d
T O P O L O G Y :   l i n e a r
M O L E C U L E   T Y P E :   p r o t e i n
U S - 0 9 - 0 4 2 - 3 5 3 - 4 8

A l i g n m e n t   S c o r e s :
P r e d .   N o . :
S c o r e :
P e r c e n t   S i m i l a r i t y :
B e s t   L o c a l   S i m i l a r i t y :
Q u e r y   M a t c h :
D B :

L e n g t h :
M a t c h e s :
C o n s e r v a t i v e :
M i s m a t c h e s :
I n d e l s :
G a p s :

1 1 7
1 0 6
3
8
0
0

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FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-042-353-48

Alignment Scores:  
Pred. No.: 2,16e-51 Length: 117  
Score: 539.00 Matches: 106  
Percent Similarity: 93.16% Conservative: 3  
Best Local Similarity: 90.60% Mismatches: 8  
Query Match: 77.22% Indels: 0  
DB: 4 Gaps: 0

US-08-728-463B-206 (1-388) x US-09-042-353-48 (1-117)

Qy 1 ATGACATGATGGTCCCGCTCAGCTCTGTGGGGTCCTGCTGCTGTGTTCCAGGTTCC 120  
Db 1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCysPheProGlyAla 20  
Qy 61 AGATGCCACATCCAGATGACCAGCTCCATCTTCCTGGTGCTGCATCTGTAGAGACAGA 120  
Db 21 ArgCysaspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
Qy 121 GTCAACCATCACTTGTGGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCCTGGTATCAGCAT 180  
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGln 60  
Qy 181 AAACACGGGAAGCCCCTAAGCTCCTGATCTATGCTGATCCAGTTGCAAAGTGGGGTC 240  
Db 61 LysProGluLysAlaProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80  
Qy 241 CCATCAAGGTTACGGGCGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300  
Db 81 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
Qy 301 CAGCTCAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCC 351  
Db 101 GlnProGluaspPheAlaThrTyrCysGlnGlnTyrAsnserTyrPro 117

RESULT 8  
US-08-758-417A-313  
Sequence 313, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP



```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-80

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Alignment Scores:		
Pred. No.:	2,798-50	Length:
Score:	529.00	Matches:
Percent Similarity:	88.19%	Conservative:
Best Local Similarity:	81.10%	Mismatches:
Query Match:	75.79%	Indels:
DB:	4	Gaps:
		0
		0
		15
		9
		103
		128

US-08-728-463B-206 (1-388) x US-08-569-147-80 (1-128)

QY		7	ATGATGGTCCCGCTCAGCTCTGTGGGGCTCTGTGTTGCCAGGTTCACGATGC	66
Db		1	MetSerValProThrGlnValLeuGlyLeuLeuLeuTrpLeuThrAspAlaArgCys	20
QY		67	GACATCCAGATGACCAGTCTCCATCTTCGTGTCATCTGTGAGGAGACAGAGTCACC	126
Db		21	AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr	40
QY		127	ATCACATTGTGGCGGAGTCAGAGTATTACGACCTGGTTAGCCTGTTATCAGCATAAACCA	186
Db		41	IleThrCysArgAlaSerGluasnIleTySerAsnLeualaTrpTyGlnGlnLysPro	60
QY		187	GGGAAGCCCCTAAGCTCTGTATGCTGCATCCAGTTTGCAAAGTGGGTCCCACATCA	246
Db		61	GlyLysAlaProLysLeuLeuIleTyfAlaalaSerAsnLeualaAspGlyValProser	80
QY		247	AGGTTTCAGCGGAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCGTCGAGCCT	306
Db		81	ArgPheSerGlyserGlyserGlyThrAspPheThrLeuThrIleSerLeuGlnPro	100
QY		307	GAAGATTTTTGCAACTTACTATTGTCACACAGGCTAATAATGTTCCCGTACACTTTTGGCCAG	366
Db		101	GluaspPheAlaThrTyfTyfCysGlnHisPheThrPrpThrProTrpAlaPheGlyGln	120
QY		367	GGGACCAAGCTGGAGATCAAA	387
Db		121	GlyThrLysValGluIleLys	127

## RESULT, T 12.

US-08-621-751A-6  
; Sequence 6, Application US/08621751a  
; Patent No. 5882644  
; GENERAL INFORMATION:  
; APPLICANT: Chang N.  
; APPLICANT: Landolfi, Nicholas P.  
; APPLICANT: Martin, Ulrich  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER LLP  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/621,751a  
; FILING DATE: 22-MAR-1996  
; CLASSIFICATION:







Db 101 GlyThrLysValGluIleLys 107

## RESULT 15

US-08-437-642B-3

Sequence 3, Application US/08437642B

Patent No. 6054297

## GENERAL INFORMATION:

APPLICANT: Paul J. Carter

APPLICANT: Leonard G. Presta

TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,642B

FILING DATE: 09-May-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934373

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05126

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-437-642B-3

## Alignment Scores:

Pred. No.:	5.56e-49	Length:	109
Score:	517.00	Matches:	99
Percent Similarity:	97.20%	Conservative:	5
Best Local Similarity:	92.52%	Mismatches:	3
Query Match:	74.07%	Indels:	0
DB:	3	Gaps:	0

US-08-728-463B-206 (1-388) x US-08-437-642B\*3 (1-109)

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGTCATCTAGGACAGAGTCCACC 126

Db 1 AspiledlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20

QY 127 ATCACTTTCGGCGAGTCCAGATATTACAGCTGGTGTAGCTGGTATCAGCATAAACCA 186

Db 21 IleThrCysArgAlaSerGlnAspValSerSerTyrLeuAlaTyrGlnGlnLysPro 40

QY 187 GGGAAAGCCCTAAGCTCTGATCTATGTCATCCAGTTTCCAAAGTGGGGTCCCATCA 246



QY 187 GGCCTGGAGTGGGATCATCTATCTGGTGAAGTCTGATACCATACAGCCGTC 246  
 Db GlyLeuGluTrpMetGlyLeuLeuValThrPheSerAspThrArgTyrSerProSer 80  
 QY 247 TTCACAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGTCACGTCG 306  
 Db PheGlnGlyGlnValThrLeuSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100  
 QY 307 AGCAGCCTGAAGGCTCGGACACCCGATGATTACTGTGGAGAGAC----- 354  
 Db SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgSerIleSerSer 120  
 QY 355 ---CAACTGGGCTCTTTGACTACTGGGGCCAGGAAACCCCTGGTCACCGTCTCTCA 408  
 Db 121 GlyTyrTyrSerAsnPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 139

## RESULT 2

PH1559

Ig heavy chain V region (clone HAN) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000

C:Accession: PH1559

R:Rassenti, L.Z.; Kippes, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1559

A:Molecule type: DNA

A:Residues: 1-136 &lt;RAS&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-115/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	1,07e-41	Length:	136
Score:	630.00	Matches:	123
Percent Similarity:	90.44%	Conservative:	0
Best Local Similarity:	90.44%	Mismatches:	11
Query Match:	74.47%	Indels:	2
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1559 (1-136)

QY 7 TCACCGCCATCTCGCCCTCTCTGGTGTCTTCCAGGAGTCTGTGCCGAGTGCAG 66  
 Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20  
 QY 67 CTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAG 126  
 Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40  
 QY 127 GGTCTGGATACAGCTTTACCGGCTACTGGATCGGTCGGCCAGATGCCCGGAAA 186  
 Db 41 GlySerArgTyrSerPheThrSerTyrTrpIleGlyTyrValArgGlnMetProGlyLys 60  
 QY 187 GGCCTGGATGGAGTGGATCATCTATCTGGTGAAGTCTGTGATACCATACAGCCGTC 246  
 Db 61 GlySerArgTyrSerPheThrSerTyrTrpIleGlyTyrValArgGlnMetProGlyLys 40  
 QY 247 TTCACAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGTCACGTCGAGTGG 306  
 Db 81 PheGlnGlyGlnValThrPheSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100  
 QY 307 AGCAGCCTGAAGGCTCGGACACCCGATGATTACTGTGGAGAGAC-----GACCAACTG 360  
 Db 101 SerArgLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuTyrGlyAspPhe 120  
 QY 361 GGCCTCTTTGACTACTGGGGCCAGGAAACCCCTGGTCACCGTCTCTCTCA 408  
 Db 121 SerThrValAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 136

## RESULT 3

PH1562

Ig heavy chain V region (clone HOW) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000

C:Accession: PH1562

R:Rassenti, L.Z.; Kippes, T.J.

J. Exp. Med. 177, 1039-1046, 1993

A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph

A:Reference number: PH1557; MUID:93210459; PMID:7681468

A:Accession: PH1562

A:Molecule type: DNA

A:Residues: 1-137 &lt;RAS&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-115/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	8,52e-41	Length:	137
Score:	618.50	Matches:	122
Percent Similarity:	90.51%	Conservative:	2
Best Local Similarity:	89.05%	Mismatches:	10
Query Match:	73.11%	Indels:	3
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1562 (1-137)

QY 7 TCACCGCCATCTCGCCCTCTCTGGTGTCTTCCAGGAGTCTGTGCCGAGTGCAG 66  
 Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20  
 QY 67 CTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAG 126  
 Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40  
 QY 127 GGTCTGGATACAGCTTTACCGGCTACTGGATCGGTCGGTCGCGCAGATGCCCGGAAA 186  
 Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleSerTyrValArgGlnMetProGlyLys 60  
 QY 187 GGCCTGGAGTGGATGGGATCATCTATCTGGTGAAGTCTGTGATACCATACAGCCGTC 246  
 Db 61 GlyLeuGluTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80  
 QY 247 TTCACAGCCAGGTCACCATCTCAGCCGACAGTCCATCAGCAGCCGTCACGTCGAGTGG 306  
 Db 81 PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100  
 QY 307 AGCAGCCTGAAGGCTCGGACACCCGATGATTACTGTGGAGAGAC----- 357  
 Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgGluGlnTrpLeuVal 120  
 QY 358 CTGGGCTCTTTGACTACTGGGGCCAGGAAACCCCTGGTCACCGTCTCTCTCA 408  
 Db 121 LeuSerAsnPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 137

## RESULT 4

E41287

Ig heavy chain precursor V-V region (257-D) (anti-HIV-1) - human

C:Species: Homo sapiens (man)

C:Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 21-Jan-2000

C:Accession: E41287

R:Andris, J.S.; Johnson, S.; Zolla-Pazner, S.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 88, 7783-7787, 1991

A:Title: Molecular characterization of five human anti-human immunodeficiency virus type

A:Reference number: A41287; MUID:91352074; PMID:1909030

A:Accession: E41287

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-144 &lt;AND&gt;

A:Cross-references: GB:M67504; NID:g185413; PIDN:AA52946.1; PID:g185414

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;



```

Db      21  LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40
Qy      127 GGTCTGGATACAGCTTTACCGCTACTGGATCGGTGGTGGCCAGAGTCCCGGAAA 186
Db      41  GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60
Qy      187 GGCCTGGAGTGGGATCATCTATCTGTGACTCTGTGATACCATACACAGCCGCTCC 246
Db      61  GlyLeuGluTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
Qy      247 TTCCAAGGCCAGGTACACCATCTCAGCCGACAAAGTCCATCAGCAGCCGCTACTCTGAGTGG 306
Db      81  PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
Qy      307 AGCAGCTGAAGCCTCGACACCCGCCATGTATTACTGTGGCAGAGACCAACTGGGCTC 366
Db      101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisThrProThrLeu 120
Qy      367 -----TTTGACTACTGGGGCCAGGAAACCCCTGGTCAACGCTCTCTCA 408
Db      121 TyrTyrTyrGlyPheAspSerTrpGlyGlnGlyThrLeuValThrValSerSer 138

RESULT 7
A28846
Ig heavy chain precursor V region (VH251) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
R:Humphries, C.G.; Shen, A.; Kuziel, W.A.; Capra, J.D.; Blattner, F.R.; Tucker, P.W.
Nature 331, 446-449, 1988
A:Title: A new human immunoglobulin V-H family preferentially rearranged in immature B-cells
A:Reference number: A28846; MUID:88122615; PMID:3123998
A:Accession: A28846
A:Molecule type: DNA
A:Residues: 1-117 <HUM>
A:Note: the authors translated the codon ATC for residue 89 as His
R:Shen, A.; Humphries, C.; Tucker, P.; Blattner, F.
Proc. Natl. Acad. Sci. U.S.A. 84, 8563-8567, 1987
A:Title: Human heavy-chain variable region gene family nonrandomly rearranged in families
A:Reference number: A39982; MUID:98068629; PMID:3120193
A:Accession: A39982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <SHE>
A:Cross-references: GB:M18806; NID:G185574; PIDN:AAA53013.1; PID:G567178
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 5.97e-39 Length: 117
Score: 595.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 70.33% Indels: 0
DB: 2 Gaps: 0

US-08-728-463b-207 (1-462) x A28846 (1-117)

Qy      1  ATGGGTCAACGCCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAG 60
Db      1  MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaIleLeuGlnGlyValCysAlaGlu 20
Qy      61  GTGCAGCTGGTCTGAGTCTGGAGCAGAGTGTAAGGAGGAGTCTCTGAAGATCTCC 120
Db      21  ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIleSer 40
Qy      121 TGTAAAGGTTCTGGATACAGCTTTTACCGCTACTGGATCGGTGGTGGCCAGAGTCC 180
Db      41  CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetPro 60
Qy      181 GGAAGGCCGTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGATACCATACAGC 240

```

```

Db      61  GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80
Qy      241 CCCTCTCTTCAAGGCCAGGTCCACCATCTCAGCCGACAAAGTCCATCAGACCCGCTACCTG 300
Db      81  ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100
Qy      301 CAGTGGAGCAGCTGAAGCCCTCGGACACCCGCTATCTATTACTGTGCGAGA 351
Db      101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117

RESULT 8
PH1564
Ig heavy chain V region (clone ANG) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jan-2000
R:Rassenti, L.Z.; Kipps, T.J.
J. Exp. Med. 177, 1039-1046, 1993
A:Title: Lack of extensive mutations in the VH5 genes used in common B cell chronic lymphocytic leukemia
A:Reference number: PH1557; MUID:93210459; PMID:7681468
A:Accession: PH1564
A:Molecule type: DNA
A:Residues: 1-138 <RAS>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8.45e-39 Length: 138
Score: 593.00 Matches: 118
Percent Similarity: 87.68% Conservative: 3
Best Local Similarity: 85.51% Mismatches: 13
Query Match: 70.09% Indels: 4
DB: 2 Gaps: 1

US-08-728-463b-207 (1-462) x PH1564 (1-138)

Qy      7  TCACCGCCATCTCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAGTGCAG 66
Db      1  SerThrAlaIleLeuAlaLeuLeuLeuAlaLeuGlnGlyValCysAlaGluValGln 20
Qy      67  CTGCTGAGTCTGGAGCAGAGGTGAAAGCCGCGGAGTCTCTGAAGATCTCTCTTAAG 126
Db      21  LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40
Qy      127 GGTCTCTGATACAGCTTTTACCGCTACTCGATCGGTGGTGGCCAGATGCCGGGAAA 186
Db      41  GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60
Qy      187 GGCCTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGTATACCATACAGCCGCTCC 246
Db      61  GlyLeuGluTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
Qy      247 TTCCAAGGCCAGGTACACCATCTCAGCCGACAAAGTCCATCAGCAGCCGCTACTCTGAGTGG 306
Db      81  PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
Qy      307 AGCAGCTGAAGCCTCGGACACCCGCTATCTATTACTGTGCGAGAGACCAACTGGGCTC 366
Db      101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisThrValGly 120
Qy      367 TTT-----GACTACTGGGCCGAGGAAACCCCTGGTCAACGCTCTCTCA 408
Db      121 TyrSerGlyCysSerGlnSerTrpGlyGlnGlyThrLeuValThrValSerSer 138

RESULT 9
PH1557
Ig heavy chain V region (clone 5-2R1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 16-Aug-1996
A:Accession: PH1557
R:Rassenti, L.Z.; Kipps, T.J.

```

J. Exp. Med. 177, 1039-1046, 1993  
A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph  
A:Reference number: PH1557; MUID:93210459; PMID:7681468  
A:Accession: PH1557  
A:Molecule type: DNA  
A:Residues: 1-115 <RAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1,47e-38 Length: 115  
Score: 590.00 Matches: 113  
Percent Similarity: 98.26% Conservative: 0  
Best Local Similarity: 98.26% Mismatches: 2  
Query Match: 69.74% Indels: 0  
DB: 2 Gaps: 0

US-08-728-463B-207 (1-462) x PH1557 (1-115)

```
QY 7 TCACCGCCATCTCGCCCTCTCTGGCTGTTCTCCAAAGGAGTCTGTCCCGAGTGCAG 66
|
|
|
Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
|
|
|
QY 67 CTGGTGCACTCTGGACGACAGGTGAAGCCCGGGAGTCTCTGAAGATCTCTCTTAAG 126
|
|
|
Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40
|
|
|
QY 127 GGTTCCTGGATACAGCTTTACCGCTACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 186
|
|
|
Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetProGlyLys 60
|
|
|
QY 187 GGCCTGGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATACAGCCCGTCC 246
|
|
|
Db 61 GlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSerProSer 80
|
|
|
QY 247 TTCACAGCCAGTCACTATCTCAGCCGACAGTCCATCAGACCCCTACCTGACGTGG 306
|
|
|
Db 81 PheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
|
|
|
QY 307 AGCAGCTGAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGA 351
|
|
|
Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 115
```

#### RESULT 10

PH1561  
Ig heavy chain V region (clone CAV) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000  
C:Accession: PH1561  
R:Rassenti, L.Z.; Kipps, T.J.  
J. Exp. Med. 177, 1039-1046, 1993  
A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymph  
A:Reference number: PH1557; MUID:93210459; PMID:7681468  
A:Accession: PH1561  
A:Molecule type: DNA  
A:Residues: 1-147 <RAS>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,71e-38 Length: 147  
Score: 586.50 Matches: 117  
Percent Similarity: 81.63% Conservative: 3  
Best Local Similarity: 79.59% Mismatches: 14  
Query Match: 69.33% Indels: 13  
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x PH1561 (1-147)

```
QY 7 TCACCGCCATCTCGCCCTCTCTGGCTGTTCTCCAAAGGAGTCTGTCCCGAGTGCAG 66
|
|
|
```

```
Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20
|
|
|
QY 67 CTGGTGCACTCTGGACGACAGGTGAAGCCCGGGAGTCTCTGAAGATCTCTCTTAAG 126
|
|
|
Db 21 LeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSerCysLys 40
|
|
|
QY 127 GGTTCCTGGATACAGCTTTACCGCTACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 186
|
|
|
Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleSerTyrPvalArgGlnMetProGlyLys 60
|
|
|
QY 187 GGCCTGGAGTGGATGGGATCATCTATCTCTGTGACTCTGTATACCATACAGCCCGTCC 246
|
|
|
Db 61 GlyLeuGlnTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80
|
|
|
QY 247 TTCACAGCCAGTCACTATCTCAGCCGACAGTCCATCAGACCCCTACCTGACGTGG 306
|
|
|
Db 81 PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100
|
|
|
QY 307 AGCAGCTGAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGAGACCAACTGGGCCCTC 366
|
|
|
Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgGlnIleAlaGlyIle 120
|
|
|
QY 367 -----TTTGACTACTTGGGGCCAGGGA 387
|
|
|
Db 121 AlaAlaAlaGlyMetTrpGlyProTyrTyrTyrTyrMetAspValTrpGlyLysGly 140
|
|
|
QY 388 ACCCTGGTCACCGTCTCTCTCA 408
|
|
|
Db 141 ThrThrValThrValSerSer 147
```

#### RESULT 11

A49047  
Ig heavy chain V region (monoclonal striational autoantibody StrAB SA-1A VH) - human (f  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998  
C:Accession: A49047  
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes  
A:Reference number: A49047; MUID:92387224; PMID:1516616  
A:Accession: A49047  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-136 <VIC>  
A:Experimental source: thymic B lymphocytes  
A>Note: sequence extracted from NCBI backbone (NCBIN:113206, NCBI:P:113207)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:19-102/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 3,92e-38 Length: 136  
Score: 584.50 Matches: 111  
Percent Similarity: 83.82% Conservative: 3  
Best Local Similarity: 81.62% Mismatches: 7  
Query Match: 69.03% Indels: 15  
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x A49047 (1-136)

```
QY 46 GGAGTCTGTCCGAGTGCAGCTGTGCTGAGCAGAGGTGAAGAGCCCGGGAG 105
|
|
|
Db 1 GlyValCysAlaGluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlu 20
|
|
|
QY 106 TCTCTGAAGATCTCTGTAAAGGTTCTTGATACAGCTTTACCGGTACTGGATCGGCTCG 165
|
|
|
Db 21 SerLeuLysIleSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrp 40
|
|
|
QY 166 GTGCGCCAGATGCCCGGAAAGCCCTGGAGTGGATCATCTATCTCTGGTACTCT 225
|
|
|
Db 41 ValArgGlnMetProGlyLysGlyLeuGluTyrMetGlyIleIleTyrProGlyAspSer 60
|
|
|
QY 226 GATACCATACAGCCCGTCTTCCAGGCCAGGTACCATCTCAGCCCAAGTCCATC 285
|
|
|
```

Db 61 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 80  
 QY 286 AGCACCGCTTACCTGAGTGGAGCAGCTGAGAGGCTCGGACCGCCATGATTACTGT 345  
 Db 81 SerThrAlaTyrLeuGlnTrpSerLeuLysAlaSerAspThrAlaMetTyrTyrCys 100  
 QY 346 GCGAGAGACCAACTGGGCTCTTTGACTAC----- 375  
 Db 101 AlaArgGlnSerTyrGlyTyrTyrAspPheAsgSerGlyTyrTyrProAlaTyrTyrTyr 120  
 QY 376 -----TGGGCGCAGGAGAACCTGCTCAGCTCTCTCA 408  
 Db 121 TyrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 136  
 RESULT 12  
 S31685  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
 C:Accession: S31685  
 R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31685  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-141 <CUI>  
 A:Cross-references: EMBL:Z14183; NID:G31033; PIDN:CAA78552.1; PID:G31034  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>  
 Alignment Scores:  
 Pred. No.: 3,98-38 Length: 141  
 Score: 584.50 Matches: 117  
 Percent Similarity: 85.82% Conservative: 4  
 Best Local Similarity: 82.98% Mismatches: 15  
 Query Match: 69.09% Indels: 5  
 DB: 2 Gaps: 2  
 US-08-728-463B-207 (1-462) x S31685 (1-141)  
 QY 1 ATGGGGTCAACCGCATCTCGCCCTCTCTGGCTGTTCTCCAAGGAGTCTGTGCGGAG 60  
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20  
 QY 61 GTCAGCTGTGAGTGTGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSer 40  
 QY 121 TGTAAGGGTCTTGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCGCCAGATGCC 180  
 Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpAlaArgGlnMetPro 60  
 QY 181 GGAAGAGGCTGAGTGGATGGGATCACTATCTCTGTGACTCTGATACCATACATACAGC 240  
 Db 61 GlyLysGlyLeuGlnTrpMetGlyArgIleAspProSerAspProTyrThrAsnTyrSer 80  
 QY 241 CCCTCTCTCCAGGCGCAGTCCACCATCTCAGCGGCAAGTCCATCAGCACCGCTTACCTG 300  
 Db 81 ProSerPheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100  
 QY 301 CAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGTTACTGTGCGGAGAGACCACTG 360  
 Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisGlyVal 120  
 QY 361 ---GGCTCTTT-----GACTACTGGGCGCAGGAAACCTGTGTCACCGTCTCC 405  
 Db 121 ArgGlyTyrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrThrValThrValSer 140  
 QY 406 TCA 408  
 |||

Db 141 Ser 141  
 RESULT 13  
 PH1563  
 Ig heavy chain V region (clone PET) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 21-Jan-2000  
 C:Accession: PH1563  
 R:Rassenti, L.Z.; Kippes, T.J.  
 J. Exp. Med. 177, 1039-1046, 1993  
 A:Title: Lack of extensive mutations in the VHS genes used in common B cell chronic lymphoma  
 A:Reference number: PH1557; MUID:93210459; PMID:7681466  
 A:Accession: PH1563  
 A:Molecule type: DNA  
 A:Residues: 1-144 <RAS>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:32-115/Domain: immunoglobulin homology <IMM>  
 Alignment Scores:  
 Pred. No.: 6,118-38 Length: 144  
 Score: 582.00 Matches: 117  
 Percent Similarity: 82.64% Conservative: 2  
 Best Local Similarity: 81.25% Mismatches: 15  
 Query Match: 68.73% Indels: 10  
 DB: 2 Gaps: 1  
 US-08-728-463B-207 (1-462) x PH1563 (1-144)  
 QY 7 TCAACCGCATCTCGCCCTCTCTGGCTGTTCTCCAAGGAGTCTGTGCGGAGTGCAG 66  
 Db 1 SerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGluValGln 20  
 QY 67 CTGTGCTGAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCTCTGAAG 126  
 Db 21 LeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuArgIleSerCysLys 40  
 QY 127 GGTCTGTGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCGGAGATGCCGGGAAA 186  
 Db 41 GlySerGlyTyrSerPheThrSerTyrTrpIleSerTrpValArgGlnMetProGlyLys 60  
 QY 187 GGCCTGAGTGGATGGGATCACTATCTGTGCTGACTCTGATACCATACAGCCCGTCC 246  
 Db 61 GlyLeuGlnTrpMetGlyArgIleAspProSerAspSerTyrThrAsnTyrSerProSer 80  
 QY 247 TTCCAAGCCAGGTCACCATCTCAGCGCAGCAAGTCCATCAGCACCGCTTACCTGCGAGTGG 306  
 Db 81 PheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeuGlnTrp 100  
 QY 307 AGCAGCTGAAGCCCTCGGACACCGCATGTTACTGTGCGGAGAGACCAACTGGGC--- 363  
 Db 101 SerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuLeuTyrGlyAla 120  
 QY 364 -----CTCTTTGACTACTGGGCGCAGGAAACCTGTGTC 396  
 Db 121 AlaAlaAlaTrpGlyTyrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrThrVal 140  
 QY 397 ACCGTCTCTCTCA 408  
 Db 141 ThrValSerSer 144  
 RESULT 14  
 PH1414  
 Ig heavy chain V region (clone P1-54) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1414  
 R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
 J. Exp. Med. 177, 99-107, 1993  
 A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of dermatitis.  
 A:Reference number: PH1409; MUID:93115676; PMID:8418213  
 A:Accession: PH1414



**THIS PAGE BLANK (USPTO)**

A:Molecule type: mRNA

A:Residues: 1-127 &lt;VAN&gt;

A:Experimental source: PBM

A:Note: the authors translated the codon TTG for residue 119 as Met

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	2,18e-37	Length:	127
Score:	575.00	Matches:	111
Percent Similarity:	89.76%	Conservative:	3
Best Local Similarity:	87.40%	Mismatches:	7
Query Match:	67.97%	Indels:	6
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1428 (1-113)

```

QY 58 GAGGTGAGCTGGTGGAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
   |||||
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
   |||||
QY 118 TCCTGTAAGGGTCTTGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCCAGATG 177
   |||||
Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
   |||||
QY 178 CCCGGGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGACTCTGATACCATAC 237
   |||||
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
   |||||
QY 238 AGCCCGTCTCTTCCAAAGGCCAGGTCCACCATCTCAGCGGACAAAGTCCATCAGACCCGCTAC 297
   |||||
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
   |||||
QY 298 CTGCAGTGGAGCAGCTTGAAGGCTTCGGACACCGCCATGTATTACTGTCCGAGAC 351
   |||||
Db 81 LeuGlnTrpSerSerLeuLysAlaThrAspThrAlaMetTyrTyrCysAlaArgAsp 100
   |||||
QY 352 -----GACCAACTGGGCTCTTTGACTACTGGGCGGAGGAAACCTGTGTCACC 399
   |||||
Db 101 TyrGlyAspTyrGlnSerThrGlyGlyPheAspProTrpGlyGlnGlyThrLeuValThr 120
   |||||
QY 400 GTCTCTCAGCTCCACCAAG 420
   |||||
Db 121 ValSerSerAlaSerThrGln 127

```

## RESULT 15

PH1428

Ig heavy chain V region (clone VH5-1R1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 28-May-1999

C:Accession: PH1428

R:van der Stoep, N.; van der Linden, J.; Logtenberg, T.

J. Exp. Med. 177, 99-107, 1993

A:Title: Molecular evolution of the human immunoglobulin E response: High incidence of B dermatitis.

A:Reference number: PH1409; MUID:93115676; PMID:8418213

A:Accession: PH1428

A:Molecule type: mRNA

A:Residues: 1-113 &lt;VAN&gt;

A:Cross-references: GB:S51905; NID:g262690; PIDN:AAC80261.1; PID:g262691

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	9,33e-37	Length:	113
Score:	567.00	Matches:	108
Percent Similarity:	93.16%	Conservative:	1
Best Local Similarity:	92.31%	Mismatches:	4
Query Match:	67.02%	Indels:	4
DB:	2	Gaps:	1

US-08-728-463B-207 (1-462) x PH1428 (1-113)

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QY 58 GAGGTGAGCTGGTGGAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117
   |||||
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
   |||||
QY 118 TCCTGTAAGGGTCTTGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCCAGATG 177
   |||||
Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40
   |||||
QY 178 CCCGGGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGACTCTGATACCATAC 237
   |||||
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60
   |||||
QY 238 AGCCCGTCTCTTCCAAAGGCCAGGTCCACCATCTCAGCGGACAAAGTCCATCAGACCCGCTAC 297
   |||||
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80
   |||||
QY 298 CTGCAGTGGAGCAGCTTGAAGGCTTCGGACACCGCCATGTATTACTGTCCGAGAC 357
   |||||
Db 81 LeuGlnTrpSerSerLeuLysAlaThrAspThrAlaMetTyrTyrCysAlaArg----- 98
   |||||
QY 358 CTGGGCTCTTTGACTACTGGGCGGAGGAAACCTGTGTCACCCTGTCTCTCA 408
   |||||
Db 99 -----AlaPheAspValTrpGlyGlnGlyThrMetValThrValSerSer 113
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Search completed: June 3, 2003, 09:07:55

Job time : 21.5421 secs

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FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Alignment Scores:
Pred. No.: 1.4e-22 Length: 139
Score: 396.50 Matches: 76
Percent Similarity: 70.50% Conservative: 22
Best Local Similarity: 54.68% Mismatches: 38
Query Match: 46.87% Indels: 3
DB: 1 Gaps: 2

US-08-728-463B-207 (1-462) x HV07_MOUSE (1-139)
QY 1 ATGGGGTCAACGCCCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerCysIleMetLeuPheLeuAlaAlaThrAlaThrGlyValHisSerGln 20
QY 61 GTGACGCTGGTCTGAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValLysLeuSer 40
QY 121 TGTAGGGTCTGGATACAGCTTACCGCTACTCGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgPro 60
QY 181 GGGAAAGGCTGGAGTGGAGTGGGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 61 GlyArgGlyLeuGluTrpIleGlyArgIleAspProAsnSerGlyThrLysTyrAsn 80
QY 241 CGCTCTTCAAGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGCCGCTACCTG 300
Db 81 GluLysPheLysSerLysAlaThrLeuThrValLysProSerSerThrAlaTyrMet 100
QY 301 CAGTGGAGCAGCTGAGGCTCGGACCGCCATCATCTATCTACTGTCGGAGA---GACCAA 357
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrAspTyr 120
QY 358 CTGGGC-----CTCTTTGACTACTGGGCGGGAACCTGTGCTACCGTCTCTCTCA 408
Db 121 TyrGlySerSerTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 139

RESULT 2
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DE 15-JUL-1999 (Rel. 38, Last sequence update)
DE Ig heavy chain V region S43 annotation (update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell'24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSSP; P01810; 2PB1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Alignment Scores:
Pred. No.: 2.79e-22 Length: 137
Score: 392.50 Matches: 76
Percent Similarity: 70.80% Conservative: 21
Best Local Similarity: 55.47% Mismatches: 39
Query Match: 46.39% Indels: 1
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x HV11_MOUSE (1-137)
QY 1 ATGGGGTCAACGCCCATCTCGCCCTCTCTGGCTGTCTCCAGGAGTCTGTGCCGAG 60
Db 1 MetGlyTrpSerCysIleMetLeuPheLeuAlaAlaThrAlaThrGlyValHisSerGln 20
QY 61 GTGACGCTGGTCTGAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluPheValLysProGlyAlaSerValLysLeuSer 40
QY 121 TGTAGGGTCTGGATACAGCTTACCGCTACTCGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrLeuMetHisTrpValAsnGlnArgPro 60
QY 181 GGGAAAGGCTGGAGTGGAGTGGGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 61 GlyArgGlyLeuGluTrpIleGlyArgIleAspProAsnSerGlyThrLysTyrAsn 80
QY 241 CGCTCTTCAAGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGCCGCTACCTG 300
Db 81 GluHisPheArgSerLysAlaThrLeuThrValLysProSerSerThrAlaTyrMet 100
QY 301 CAGTGGAGCAGCTGAGGCTCGGACCGCCATCATCTATCTACTGTCGGAGACCACTG 360
Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrArgLeu 120
QY 361 GGC---CTCTTTGACTACTGGGCGGGAACCTGTGCTACCGTCTCTCTCA 408
Db 121 GlyArgTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 137

RESULT 3
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 93G7 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/J;  
 RX MEDLINE=82152818; PubMed=6801765;  
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
 RA "Somatic mutation in genes for the variable portion of the  
 RT immunoglobulin heavy chain."  
 RT Science 216:309-311(1982).  
 RL -----  
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 CC -----  
 DR EMBL; J00493; AAA38128.1; -.  
 DR PIR; A02028; HVM5G7.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 DR Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.  
 KW SIGNAL  
 FT CHAIN 1 19  
 FT NON\_TER 140 140 IG HEAVY CHAIN V REGION 93G7.  
 FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.44e-21 Length: 140  
 Score: 383.00 Matches: 76  
 Percent Similarity: 70.71% Conservative: 23  
 Best Local Similarity: 54.29% Mismatches: 37  
 Query Match: 45.27% Indels: 4  
 DB: 1 Gaps: 2  
 US-08-728-463B-207 (1-462) x HV02\_MOUSE (1-140)  
 QY 1 ATGGGGTCAACCGCCATCTCCGCTCTCTGCTGTTCTCAAGGAGTCTGTCCGAG 60  
 DB 1 MetGlyTrpSerPheIlePheLeuPheLeuSerValThrAlaGlyValHisSerGlu 20  
 QY 61 GTGCAGCTGGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTCC 120  
 DB 21 ValGlnLeuGlnGlnSerGlyAlaGlnLeuValArgAlaGlySerSerValHisMetSer 40  
 QY 121 TCTAAGGGTCTGGATACAGCTTTACCGCTACTGATCGGTGGTGGTGGTGGTGGTGGT 180  
 DB 41 CysLysAlaSerGlyTyrThrPheThrSerTyrGlyIleAsnTrpValLysGlnArgPro 60  
 QY 181 GGGAAAGGCTGGATGGATGGATCATCTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240  
 DB 61 GlyGlnGlyLeuGluTrpIleGlyTyrIleAsnProGlyAsnGlyTyrIleAsnTyrAsn 80  
 QY 241 CGGTCTCTCAAGGCGAGTCAACATCTCAGCGCAAGTCCATGATGATGATGATGATGATG 300  
 DB 81 GluLysPheGlyLysThrThrLeuThrValAspLysSerSerThrAlaTyrMet 100  
 QY 301 CAGTGGAGCAGCTGAAGGCTCGGACCGCATATGTTACTGTGCGGAGACCAACTG 360  
 DB 101 GlnLeuArgSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgSerHisTyr 120  
 QY 361 -----GGCCTC-----TTTGACTACTGGGGCCAGGAAACCCCTGCTACCTCTCTCA 408

Db 121 TyrGlyGlySerTyrAspPheAspTyrTrpGlyGlnGlyThrProLeuThrValSerSer 140  
 RESULT 4  
 HV01\_MOUSE  
 ID HV01\_MOUSE STANDARD; PRT; 121 AA.  
 AC P01745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region MPC 11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81053741; PubMed=6253904;  
 RA Zakut R., Cohen J., Givol D.;  
 RT "Cloning and sequence of the cDNA corresponding to the variable  
 RT region of immunoglobulin heavy chain MPC11."  
 RL Nucleic Acids Res. 8:3591-3601(1980).  
 RN [2]  
 RP REVISIONS.  
 RA Zakut R., Cohen J., Givol D.;  
 RL Nucleic Acids Res. 8:4839-4840(1980).  
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
 CC FROM A MYELOMA THAT SECRETES IGG2B.  
 CC PIR; A02027; GVMS11.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 DR Immunoglobulin V region.  
 KW NON\_TER 121 121  
 FT SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;  
 SQ  
 Alignment Scores:  
 Pred. No.: 5.72e-21 Length: 121  
 Score: 375.00 Matches: 69  
 Percent Similarity: 74.38% Conservative: 21  
 Best Local Similarity: 57.02% Mismatches: 27  
 Query Match: 44.33% Indels: 4  
 DB: 1 Gaps: 1  
 US-08-728-463B-207 (1-462) x HV01\_MOUSE (1-121)  
 QY 58 GAGTGTGAGTGTGTCAGTCTGGAGCAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117  
 DB 1 GluAlaGlnLeuGlnGlnSerGlyAlaGlnLeuValArgProGlyThrSerValLysile 20  
 QY 118 TCCTTAAGGGTCTGGATACAGCTTTACCGCTACTGATCGGTGGTGGTGGTGGTGGTGG 177  
 DB 21 SerCysLysAlaAlaGlyTyrThrPheThrAsnTyrTrpIleGlyTrpValLysGluArg 40  
 QY 178 CCCGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTTGTTGTTGTTGTTGTTGTTGTT 237  
 DB 41 ProGlyHisGlyLeuGluTrpIleGlyAspIleTyrProGlyGlyGlyPheThrAsnTyr 60  
 QY 238 AGCCCGTCTTCCAAAGGCGAGTCAACATCTCAGCGCAAGTCCATGATGATGATGATGAT 297  
 DB 61 AsnAspAsnLeuLysGlyLysAlaThrLeuThrAlaAspThrSerSerThrAlaTyr 80  
 QY 298 CTGCAAGTGGAGCAGCTCAAGGCTCGGACCGCCATGATGATGATGATGATGATGATGATG 351  
 DB 81 IleGlnLeuSerSerLeuThrSerGluAspSerAlaIleTyrHisCysAlaArgGlyIle 100  
 QY 352 -----GACCAACTGGGCTCTTTGACTACTGGGCGCCAGGAAACCCCTGCTACCGCTCTCC 405  
 DB 101 TyrTyrAsnSerSerProTyrPheAspSerTrpGlyGlnGlyThrThrLeuThrValSer 120  
 QY 406 TCA 408

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Db      121 Ser 121
RESULT 5
HV48 MOUSE
AC P0390; STANDARD; PRT; 138 AA.
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TPC 1017 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Alignment Scores:
Pred. No.: 6,79e-21 Length: 138
Score: 374.00 Matches: 72
Percent Similarity: 69.78% Conservative: 25
Best Local Similarity: 51.80% Mismatches: 38
Query Match: 44.21% Indels: 4
DB: 1 Gaps: 2

US-08-728-463b-207 (1-462) x HV48_MOUSE (1-138)
QY 1 ATGGGCTCAACCCCATCTCGCCCTCTCTGCTGTTCTCAAGAGTCTGTCCGAG 60
Db 1 MetGlyTrpSerTyrlleLeuPheLeuValAlaThrAlaThrAspValHisSerGln 20
QY 61 GTCCAGCTGGTGCAGTCTCGAGCAGAGGTGAAGAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValGlnLeuSer 40
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTCGATCGGCTGGTGGCCAGATGCC 180
Db 41 CysLysAlaSerGlyHisThrPheThrAsnTyrlleHisTrpValLysGlnArgPro 60
QY 181 GGAAGAGGCTGGAGTGGATGGGATCATCTATCTGCTGATCTGTATACACATACAGC 240
Db 61 GlyGlnGlyLeuGluTrpIleGlyGluLeuAsnProAsnAspGlyArgSerAsnTyra 80
QY 241 CGTCTCTCAAGAGGCGAGTCAACATCTCAGCCGACAGTCCATCAGCCGCTACTCTG 300
Db 81 GluLysPheLysAsnLysAlaThrLeuThrValAlaPheLysSerSerThrAlaTyMet 100

QY 301 CAGTGGAGCAGCTGAAGCCCTGGACACCCGCTGTTCTTACTGTGCGAGACCAACTG 360
Db 101 GlnLeuSerSerLeuThrProGluGluPheAlaValTyrlleValHisSerAsp 119
QY 361 GGCCTCTTTGAC-----TACTGGGCGCAGGAGAACCTGCTCACCGTCTCTCTCA 408
Db 120 GlyTyrlleAspTrpPheValTyrlleGlyGlnGlyThrLeuValThrPheSerAla 138

RESULT 6
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC PIR; A02032; HVMS02.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Alignment Scores:
Pred. No.: 1.61e-20 Length: 117
Score: 369.00 Matches: 66
Percent Similarity: 75.86% Conservative: 22
Best Local Similarity: 56.90% Mismatches: 28
Query Match: 43.62% Indels: 0
DB: 1 Gaps: 0

US-08-728-463b-207 (1-462) x HV06_MOUSE (1-117)
QY 1 ATGGGCTCAACCCCATCTCGCCCTCTCTGCTGTTCTCAAGAGTCTGTCCGAG 60
Db 1 MetGlyTrpSerCysAllelleLeuPheLeuValAlaThrAlaThrGlyValHisSerHis 20
QY 61 GTCCAGCTGGTGCAGTCTCGAGCAGAGGTGAAGAGCCCGGGAGTCTCTGAAGATCTCC 120
Db 21 ValGlnLeuGlnProGlyAlaGluLeuValLysProGlyAlaSerValLysValSer 40
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTCGATCGGCTGGTGGCCAGATGCC 180
Db 41 CysLysAlaSerGlyTyrlleThrPheThrSerTyrlleMetHisTrpValLysGlnArgPro 60
QY 181 GGAAGAGGCTGGAGTGGATGGGATCATCTATCTGCTGATCTGTATACACATACAGC 240

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Db      61 GlyGlnGlyLeuGluTrpIleGlyArgIleHisProSerAspSerAspThrAsnTyrAsn 80
Qy      241 CGTCTCCAGGCGAGTACCATCTCAGCGGAGAGTCCATCAGACGCGCTACCTG 300
Db      81 GlnLysPheLysGlyAlaThrLeuThrValAspLysSerSerThrAlaTyrMet 100
Qy      301 CAGTGGAGCAGCTCAGAGCCTCGACACCGCCATGTATTACTGTGCG 348
Db      101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrTyrCysAla 116

RESULT 7
HV1B HUMAN
ID HV1B HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RL (VH) gene subgroups."
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00240; AAA52988.1; -
DR PIR; A02024; HVH0HG.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Alignment Scores:
Pred. No.: 2,27e-20 Length: 117
Score: 367.00 Matches: 67
Percent Similarity: 78.70% Conservative: 18
Best Local Similarity: 62.04% Mismatches: 23
Query Match: 43.38% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV1B_HUMAN (1-117)

Qy      28 CTCCTGGCTGTTCTCAAGAGTCTGTGCCAGGTGCAGTCTGTCAGTCTGAGCAGAG 87
Db      10 LeuLeuAlaValAlaProGlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGlu 29
Qy      88 GTGAAAGCCGGGAGTCTCTGAGATCTCTGTAGGGTCTCGATACAGCTTTACC 147
Db      30 ValLysLysProGlyAlaSerValLysValSerCysLysAlaSerGlyTyrThrPheAsn 49
Qy      148 GCCTACTGATCGCTGGTGGTCGCGCAGATGCCCGGAAAGCCTGGAGTGGATGGGATC 207
Db      50 SerTyrTyrMetHisTrpValargGlnAlaProGlyGlnGlyLeuGluTrpMetGlylle 69

```

```

Qy      208 ATCTATCTCTGCTGACTCTGATACCATACAGCCGCTCTTCCAGGCCAGTCCACCATC 267
Db      70 IleAsnProSerGlyGlySerThrSerTyrAlaGlnLysPheGlnGlyArgValThrMet 89
Qy      268 TCAGCCGACAAAGTCCATCAGACCGCCCTACCTGAGTGGAGCAGCCTGAAGGCTCGGAC 327
Db      90 ThrArgAspThrSerThrValTyrMetGluLeuSerSerLeuArgSerGluAsp 109
Qy      328 ACCGCCATGTATTACTGTGCGAGA 351
Db      110 ThrAlaValTyrTyrCysAlaArg 117

RESULT 8
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GENE LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Alignment Scores:
Pred. No.: 2,7e-20 Length: 117
Score: 366.00 Matches: 65
Percent Similarity: 76.07% Conservative: 24
Best Local Similarity: 55.56% Mismatches: 28
Query Match: 43.26% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV05_MOUSE (1-117)

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[illegible]

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RESULT 9  
HV13 MOUSE STANDARD; PRT; 117 AA.  
ID HV13 MOUSE  
AC P01757;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE .ig heavy chain V region J558.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxId=10090;  
RN [1]  
RP SEQUENCE.  
MEDLINE=80078170; PubMed=6765983;  
Schilling J., Clevinger B., Davie J.M., Hood L.;  
RA "Amino acid sequence of homogeneous antibodies to dextran and DNA  
RR rearrangements in heavy chain V-region gene segments.";  
RT Nature 283:35-40(1980).  
RNL -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYPERDOMA PROTEINS THAT ALSO  
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT I-7 POSITIONS, MANY OF  
CCC WHICH OCCUR IN THE D AND J SEGMENTS.  
--!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
```

```

PIK; A26342; MHMSJS.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
DISULFID 22 96
NON_TER 117 117
SEQUENCE 117 AA; 13024 MW; 2992AP4BE447E41 CRC64;

BY SIMILARITY.

Alignment Scores:
Pred. No.: 2 7e-20
Score: 366.00
Percent Similarity: 75.21%
Local Similarity: 57.26%
Query Match: 43.26%
ID: 1
Gaps: 0
Indels: 0
MisMatches: 29
Conservative: 21
Matches: 67
Length: 117

```

IS-08-728-463B-207 (1-462) x HV13\_MOUSE (1-117)

58	GAGGTGCACGTGGTCACTGGACACAGAGTGAAGAAAGCCGGGGAGTCTCTGAAGATC	117
yy		
bb	1 G u v a l n e u g n s e r c y P r o l u e v a l l y s p r o g i a l s e r v a l l y s m e t	20
yy	118 TCCTGTGAAGGGTTCTGGATACAGCTTTACCGCGTACTCGGCTCGGTTGGGTGGCCACAGATG	177

[illegible]

RESULT 10	
HVIC HUMAN	
ID HVIC HUMAN	STANDARD; PRT; 147 AA.
AC P01744;	
DT 21-JUL-1986	(Rel. 01, Created)
DT 16-OCT-2001	(Rel. 40, Last sequence update)
DT 16-OCT-2001	(Rel. 40, Last annotation update)
DE lg heavy chain V-I region ND precursor (Fragmente).	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A..	
RX MEDLINE=83065234; PubMed=6815656;	
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,	
RA Bell L.O., Gould H.J.;	
RT "Cloning and sequence determination of the gene for the human	
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";	
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).	
RN [2]	
RP SEQUENCE OF 20-147.	
RQ Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;	
RL (In) Bach M.K. (eds.);	
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36	
RL Marcel Dekker, New York (1978).	
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA	

[illegible]

Alignment Scores:	
Sred. No.:	4.93e-20
Scores:	362.50
Length:	147
Matches:	71
Conservative:	22
Mismatches:	43
Indels:	11
Gaps:	1
DB:	1







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Score: 355.00 Matches: 68  
Percent Similarity: 69.8% Conservative: 27  
Best Local Similarity: 50.0% Mismatches: 41  
Query Match: 41.96% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV15\_MOUSE (1-136)

QY 1 ATGGGGTCAACCGCCATCTCGCCCTCTCTGGTGTCTTCCCAAGGAGTCTGTGCGGAG 60  
Db 1 MetGlyTrpSerCysIlellePhePheLeuValAlaThrAlaThrGlyValHisSerGln 20  
QY 61 GTGCAGCTGGTCCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
Db 21 ValGlnLeuGlnSerGlyProGluValAlaArgProGlyValSerValIleSer 40  
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTGGATCGCGTGGGTCGCCAGATGCC 180  
Db 41 CysLysGlySerGlyTyrThrPheThrAspTyrAlaMetHisTrpValLysGlnSerHis 60  
QY 181 GGGAAAGCCTGGAGTGGGATCATCTATCTCTGGTGAATCTGTATACCATACAGC 240  
Db 61 AlalysSerLeuGluTrpIleGlyValIleSerThrTyrAenGlyAenThrSerTyrAen 80  
QY 241 CCGTCTTCCAAAGCCAGGTCAACATCTCAGCCGACAGTCCATCAGCAGCCGCTACCTG 300  
Db 81 GlnLysPheLysGlyLysAlaThrMetThrValAspLysSerSerThrValHisMet 100  
QY 301 CAGTGGAGCAGCTGAAGGCTCGGACACCGCCATGTATCTGTGCGAGAGACCAACTG 360  
Db 101 GluLeuAlaArgLeuThrSerGluAaspSerAlaAenLeuTyrCysAlaArgTyrTyrGly 120  
QY 361 GGCTCTTCTACTACTGGGCGGAGAACCTGTGTACCTGTCCCTCTCTCA 408  
Db 121 AsnTyrPheAspTyrTrpGlyGlnGlyThrLeuThrValSerSer 136

RESULT 15  
HV04\_MOUSE  
ID HV04\_MOUSE STANDARD; PRT; 117 AA.  
AC P01748;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 23 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR PIR: A02030; HWS23.  
DR HSSP: P01810; 2FBU.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
DR Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Alignment Scores:  
Pred. No.: 2,54e-19 Length: 117  
Score: 353.00 Matches: 64  
Percent Similarity: 73.50% Conservative: 22  
Best Local Similarity: 54.70% Mismatches: 31  
Query Match: 41.73% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x HV04\_MOUSE (1-117)

QY 1 ATGGGGTCAACCGCCATCTCGCCCTCTCTGGTGTCTTCCCAAGGAGTCTGTGCGGAG 60  
Db 1 MetGlyTrpSerCysIlellePheLeuValAlaAalaAenGlyValHisSerGln 20  
QY 61 GTGCAGCTGGTCCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
Db 21 ValGlnLeuGlnProGlyThrGluLeuValLysProGlyAlaSerValLysLeuSer 40  
QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGCTACTGGATCGCGTGGGTCGCCAGATGCC 180  
Db 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpMetHisTrpValLysGlnArgPro 60  
QY 181 GGGAAAGCCTGGAGTGGGATCATCTATCTGTGACTCTGTATACCATACAGC 240  
Db 61 GlyGlnGlyLeuGluTrpIleGlyAenIleAenProGlyAenGlyGlyThrAsnTyrAen 80  
QY 241 CCGTCTTCCAAAGCCAGGTCAACATCTCAGCCGACAAAGTCCATCAGCCGCTACTCTG 300  
Db 81 GluLysPheLysSerLysValThrLeuThrValAspLysSerSerThrAlaTyrThr 100  
QY 301 CAGTGGAGCAGCTGAAGGCTCGGACACCGCCATGTATCTGTGCGGAG 351  
Db 101 GlnLeuSerSerLeuThrSerGluAaspSerAlaValTyrTyrCysAlaArg 117

Search completed: June 3, 2003, 09:04:05  
Job time : 10.7633 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 41.0121 Seconds

(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-207

Perfect score: 846

Sequence: 1 ATGGGGTCAACGGCCATCTT.....CACCCCTCTCCAGAGAGCTT 462

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool/US08728463/runat.03062003.085614.16815/app.query.fasta\_1.3690  
-DB=SPTRMBL 21 -QWTF-fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cui -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CGN 1 1 380 @runat.03062003.085614.16815 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archaeap:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	450	53.2	473	11	Q9D8L4 mus musculus

ID	Q9D8L4	PRELIMINARY:	PRT:	473 AA.
2	446	52.7	474	11
3	442.5	52.3	463	11
4	434	51.3	168	11
5	433.5	51.2	471	4
6	429	50.7	150	4
7	427.5	50.5	613	11
8	427	50.5	481	11
9	426	50.4	468	11
10	419.5	49.6	278	11
11	418.5	49.5	143	11
12	417.5	49.3	473	11
13	417	49.3	157	4
14	411	48.6	614	4
15	410.5	48.5	124	4
16	409.5	48.4	147	4
17	408.5	48.3	118	11
18	405	47.9	125	4
19	404	47.8	119	4
20	403	47.6	146	11
21	402	47.5	142	11
22	402	47.5	142	11
23	400.5	47.3	143	11
24	399.5	47.2	145	11
25	398.5	47.1	145	11
26	398	47.0	140	11
27	397.5	47.0	143	11
28	396.5	46.9	145	11
29	396	46.8	497	4
30	395	46.7	146	11
31	395	46.7	597	4
32	394.5	46.6	137	11
33	394.5	46.6	143	11
34	393.5	46.5	141	11
35	393.5	46.5	145	11
36	393.5	46.5	145	11
37	393.5	46.5	145	11
38	392.5	46.4	473	11
39	391.5	46.3	143	11
40	391	46.2	146	11
41	390.5	46.2	159	4
42	390.5	46.2	613	4
43	389.5	46.0	143	11
44	389	46.0	484	11
45	387.5	45.8	145	11

## ALIGNMENTS

RESULT 1

Q9D8L4  
ID Q9D8L4  
AC Q9D8L4;  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE 181006009Rik protein.  
GN IGH-1 OR 181006009RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
RX MEDLINE=21085560; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,



RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003435; AAH03435.1; -;  
 DR HSSP; P01842; 7FAB.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGH1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Alignment Scores:  
 Pred. No.: 2,83e-33 Length: 463  
 Score: 442.50 Matches: 83  
 Percent Similarity: 73.1% Conservative: 26  
 Best Local Similarity: 55.70% Mismatches: 37  
 Query Match: 52.30% Indels: 3  
 DB: 11 Gaps: 1

US-08-728-463B-207 (1-462) x Q99LC4 (1-463)

QY 16 ATCTCGCCCTCTCTGCTGCTCTTCCAAAGGAGTCTGTGCGAGGTGCGAGTGTGCGAG 75  
 DB 6 IIEPheLeuPheIleLeuSerGlyThrAlaGlyValHisSerGlnValGlnLeuGln 25  
 QY 76 TCTGGAGCAGAGTGAAGAAAGCCGGGAGTCTCTGAAGATCTCTGTAAAGGTTCTGGA 135  
 DB 26 SerGlyAlaGluLeuAlaArgProGlyAlaSerValArgLeuSerCysLysAlaSerGly 45  
 QY 136 TACAGCTTACCGGCTACTGGATCGGCTGGTGGCGCCAGATCCCGGAAAGCCCTGGAG 195  
 DB 46 TyrThrPheThrGlyTyrGlyValSerTrpValLysGlnArgThrGlyGlnGlyLeuGlu 65  
 QY 196 TGGATGGGATCATCTATCTCTGCTGCTGTATGATACACATACAGCCCGCTCTTCAAGGC 255  
 DB 66 TrpValGlyGluLeuTyrProGlySerGlyAsnThrTyrTyrSerGluLysPheLysGly 85  
 QY 256 CAGGTCAACCATCTCAGCCGACAAAGTCCATCAGACCGCTACTGTCAGTGGAGCAGCCTG 315  
 DB 86 LysAlaThrLeuThrThrAspLysSerSerSerThrAlaTyrMetHisLeuSerSerLeu 105  
 QY 316 AAGGCTCGGACACCGCCATGATTACTGTGGAGAGAC-----CAACTGGGCTCTC 366  
 DB 106 ThrSerGluAspSerAlaValTyrPheCysAlaArgSerSerTyrTyrSerTyrAspLeu 125  
 QY 367 TTTGACTACTGGGCGGAGGACCTGTGTCACCGTCTCTCAGCTTCCAGCTCCACCAAGGCCCA 426  
 DB 126 PheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaAlaLysThrThrProPro 145  
 QY 427 TCGGTCTTCCCTCGGACCTCTCTCC 453  
 DB 146 SerValTyrProLeuAlaProGlySer 154

RESULT 4

Q8VDC9 PRELIMINARY; PRT; 168 AA.  
 AC Q8VDC9;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Anti-MOG Z12 variable gamma 2a (Fragment).  
 GN IGG2A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Chernaiovsky Y.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Sembi P.;  
 RT "Targeting T cells to the CNS";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ416332; CAC94867.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR InterPro; IPR001230; Prenyl\_site.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00294; PRENYLATION; UNKNOWN 1.  
 FT NON TER 168 168  
 SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Alignment Scores:  
 Pred. No.: 1.5e-32 Length: 168  
 Score: 434.00 Matches: 82  
 Percent Similarity: 70.27% Conservative: 22  
 Best Local Similarity: 55.41% Mismatches: 42  
 Query Match: 51.30% Indels: 2  
 DB: 11 Gaps: 1

US-08-728-463B-207 (1-462) x Q8VDC9 (1-168)

QY 10 ACCGCACTCTCTGCTGCTCTTCCAAAGGAGTCTGTGCGAGGTGCGAGTGTGAGCTG 69  
 DB 4 ThrTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisSerGlnValGlnLeu 23  
 QY 70 GTGAGTCTGGAGCAGAGTGAAGAAAGCCGGGAGTCTCTGAAGATCTCTGTAAAGGT 129  
 DB 24 GlnGlnSerGlyAlaGluLeuMetLysProGlyAlaSerValLysIleSerCysLysAla 43  
 QY 130 TCTGATACAGCTTACCGGCTACTGGATCGGCTGGTGGTGGCCAGATCCCGGAAAGGC 189  
 DB 44 ThrGlyTyrThrPheSerSerTyrTrpIleAspTrpValLysGlnArgProGlyHisGly 63  
 QY 190 CTGGAGTGGAGGAGTATCTATCTCTGCTGCTGTATGATACACATACAGCCCGTCTTC 249  
 DB 64 LeuGluTrpIleGlyGluLeuProGlySerGlyArgThrAsnTyrAsnGluLysPhe 83  
 QY 250 CAAGCCAGGTCAACCATCTCAGCCGACAAAGTCCATCAGACCGCTCTCTGAGTGGAGC 309  
 DB 84 LysGlyLysThrThrPheThrAlaAspThrSerSerAsnThrAlaTyrIleGlnPheSer 103  
 QY 310 AGCTGAAGGCTCGGACACCGCATGATTACTGTGGAGA-----GACCACTGGGC 363  
 DB 104 SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaAsnTyrGlySerSerArgTrp 123  
 QY 364 CTCTTTGACTACTGGGCGGAGGACCTGTGTCACCGTCTCTCAGCTCTCCACCAAGGC 423  
 DB 124 TyrPheAspValTrpGlyAlaGlyThrValThrValSerSerThrLysThrThrAla 143  
 QY 424 CCATCGGTCTTCCCTCGGACCC 447  
 DB 144 ProSerValTyrProLeuAlaPro 151

RESULT 5

Q8TC77 PRELIMINARY; PRT; 471 AA.  
 AC Q8TC77;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Hypothetical 51.8 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC024289; AAH24289.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 471 AA; 51791 MW; 388774CF588660E CRC64;

Alignment Scores:  
 Pred. No.: 28-32 Length: 471  
 Score: 433.50 Matches: 86  
 Percent Similarity: 73.65% Conserv: 23  
 Best Local Similarity: 58.11% Mismatches: 34  
 Query Match: 51.24% Indels: 5  
 DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x Q8TC77 (1-471)

QY 28 CTCCTGGCTGTCTCCAGGAGTCTGTCAGGAGTCTGTCAGTCTGAGTCTGAGCAGAG 87  
 Db 10 LeuValAlaLeuLeuGluGlyValGlnCysGluValGlnLeuValGluSerGlyGly 29  
 QY 88 GTGAAAGCCCGGGAGTCTCTGAAGATCTCTCTGTAAGGTTCTGGATACAGCTTACC 147  
 Db 30 LeuValLysProGlyGlySerLeuArgLysSerCysAlaLaserGlyPheThrPheSer 49  
 QY 148 GCCTACTGATCGCTGGTCCGAGTCCAGATCCCGGAAAGCCCTGAGTGGGATC 207  
 Db 50 SerTyrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValSer 69  
 QY 208 ATCTATCTGTGTGATCTGTATACATACAGCCGCTCTCCAGGCCAGGTCCACATC 267  
 Db 70 MetSerSerSerSerTyrIleTyrTyrAlaAspSerValLysGlyArgPheThrIle 89  
 QY 268 TCAGCCGACAGTCCATCAGCAGCCGCTACTCGATGGAGAGCTGAGGCTCGGAC 327  
 Db 90 SerArgAspAlaLysAsnSerLeuTyrLeuGlnMetAsnSerLeuArgAlaGluAsp 109  
 QY 328 ACCGCCATGTACTGTGCGAGAGACCACTGGGCTC-----TTGAC 372  
 Db 110 ThrAlaValTyrTyrCysAlaAaGAspLeuArgGlnLeuThrSerTyrTrpTyrPheAsp 129  
 QY 373 TACTGGGCGAGGACCCCTGGTCCAGTCTCTCAGCTCCAGCTCCAGGCGCCATCGGTC 432  
 Db 130 LeuTrpGlyArgGlyThrLeuValThrValSerAlaSerThrLysGlyProSerVal 149  
 QY 433 TTCCCTCTGGCACCCTCTCCCAAG 456  
 Db 150 PheProLeuAlaProSerSerLys 157

RESULT 6

ID Q9Y298 PRELIMINARY; PRT; 150 AA.  
 AC Q9Y298;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IGG VH protein precursor (Fragment).  
 GN IGG VH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98322155; PubMed=9657749;  
 RA Jacquemin M.G., Vander Elst L.P.L.;

RT "Mechanism and kinetics of factor VIII inactivation: study with an  
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with  
 RT inhibitor.";  
 RL Blood 92:496-506(1998).  
 DR EMBL; AJ224083; CAA11829.1; -;  
 DR HSP; P01772; 2F84.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT NON\_TER 150 150  
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Alignment Scores:  
 Pred. No.: 4-36e-32 Length: 150  
 Score: 429.00 Matches: 83  
 Percent Similarity: 72.34% Conserv: 19  
 Best Local Similarity: 58.87% Mismatches: 39  
 Query Match: 50.71% Indels: 0  
 DB: 4 Gaps: 0

US-08-728-463B-207 (1-462) x Q9Y298 (1-150)

QY 19 CTCGCCCTCTCTCTGGCTGTCTCCAGGAGTCTGTCAGGAGTCTGTCAGTCTGAGTCT 78  
 Db 7 IleLeuPheLeuValAlaAlaAlaThrGlyThrHisAlaGlnValGlnLeuValGlnSer 26  
 QY 79 GGAGCAGAGGTGAAGAAAGCCCGGGAGTCTCTGAAGATCTCTGTAAGGTTCTGGATAC 138  
 Db 27 GlyAlaGluValLysProGlyAlaSerValLysValSerCysLysValSerGlyTyr 46  
 QY 139 AGCTTTACCGCTACTCGATCGGCTGGTGGTGGCAGATCCCGGAAAGCCCTGAGTGG 198  
 Db 47 ThrLeuThrGluLeuProValHisTrpValGlyGlnAlaProGlyLysGlyLeuGluTrp 66  
 QY 199 ATGGGGATCATCTATCTGTGTGACTCTGTATACATACAGCCGCTCTCCAGGCCAG 258  
 Db 67 ValGlySerPheAspProGluSerGlyGluSerIleTyrAlaArgGluPheGlnGlySer 86  
 QY 259 GTACACATCTCAGCCGACAAAGTCCATCAGCAGCCGCTACTCGATGGAGCAGCTGAAG 318  
 Db 87 ValThrMetThrAlaAspThrSerThrAspIleAlaTyrMetGluLeuSerSerLeuArg 106  
 QY 319 GCCTCGGACACCCCACTGTATTACTGTGCGAGAGACCAACTGGGCTCTTTGACTACTGG 378  
 Db 107 SerAspAspThrAlaValTyrCysAlaValProAspProAspAlaPheAspIleTrp 126  
 QY 379 GGCCAGGGAACCTGTCTACCCGTCTCTCAGGCTCCACCAAGGCCCATCGCTTCCCC 438  
 Db 127 GlyGlnGlyThrMetValThrValSerSerAlaSerThrLysGlyProSerValPhePro 146  
 QY 439 CTG 441  
 Db 147 Leu 147

RESULT 7

ID Q8VCX7 PRELIMINARY; PRT; 613 AA.  
 AC Q8VCX7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 67.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN; GLAND;  
 RA Strausberg R.;



RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018315; AAH18315.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 5.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DDA22862 CRC64;

## Alignment Scores:

Pred. No.: 7,71e-32 Length: 613  
 Score: 427.50 Matches: 86  
 Percent Similarity: 69.87% Conservative: 23  
 Best Local Similarity: 55.13% Mismatches: 40  
 Query Match: 50.53% Indels: 7  
 DB: 11 Gaps: 3

US-08-728-463B-207 (1-462) x Q8VCX7 (1-613)

QY 10 ACCGCCATCTCGCCCTCTCTGGTGTCTCCAGGAGTCTGTGCCAGGTGCAGTGTG 69  
 DB 4 ThrTrpValPheLeuPheLeuSerValThrAlaGlyValHisSerGlnValGlnLeu 23  
 QY 70 GTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTCAAGATCTCTGTAAGGT 129  
 DB 24 GlnGlnSerGlyAlaGlnLeuMetLysProGlyAlaSerValLysIleSerCysLysAla 43  
 QY 130 TCTGATACAGCTTTACCGGCTACTGGATCGGTGGTGGCCAGATGCCCGGAAAGGC 189  
 DB 44 ThrGlyTyrThrPheSerSerTyrTrpIleGluTrpValLysGlnArgProGlyHisGly 63  
 QY 190 CTGGAGTGTGGATGGGATCATCTCTGGTGTACTGTGATCTGTATACACATACAGCCGCTCTTC 249  
 DB 64 LeuGluTrpIleGlyGluLeuProGlySerGlySerThrAsnTyrAsnGlnLysPhe 83  
 QY 250 CAAGGCCAGGTCAACATCTCAGCCAGCAAGTCCATCAGCAGCCGCTACTCTGAGTGGAGC 309  
 DB 84 LysGlyLysAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeuSer 103  
 QY 310 AGCTTGAAGCTTCGGACACCCCATGTATTACTGTGGAGAGACCAACTGGCC----- 363  
 DB 104 SerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArg---ArgLeuGlyArgTrp 122  
 QY 364 CTCTTGACTACTGGCCAGGAGACCTGGTCCAGCTCTCTCAGCTCCACCAAGGC 423  
 DB 123 TyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSerGlnSerPhe 142  
 QY 424 CCATCGTCTCTCCCTCG-----GCACCTCTCTCAAGAAG 459  
 DB 143 ProAsnValPheProLeuValSerCysGluSerProLeuSerAspLys 158

## RESULT 8

Q91WT1 PRELIMINARY; PRT; 481 AA.  
 AC Q91WT1;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Hypothetical 52.1 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COLON;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013490; AAH13490.1; -.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; IG; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

## Alignment Scores:

Pred. No.: 8.24e-32 Length: 481  
 Score: 427.00 Matches: 80  
 Percent Similarity: 72.11% Conservative: 26  
 Best Local Similarity: 54.42% Mismatches: 41  
 Query Match: 50.47% Indels: 0  
 DB: 11 Gaps: 0

US-08-728-463B-207 (1-462) x Q91WT1 (1-481)

QY 1 ATGGGGTCAACCGCATCTCGCCCTCTGGTGTCTTCCAGGAGTCTGTGCCGAG 60  
 DB 1 MetGlyTrpArgTrpIlePheLeuPheLeuSerGlyThrAlaGlyValGlnCysGln 20  
 QY 61 GTGCAGTCTGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
 DB 21 ValGlnLeuLeuGlnSerGlyProGluLeuValLysProGlyAlaSerValLysIleSer 40  
 QY 121 TGTAGGGTCTTGATACAGCTTTACCGGCTACTGGATCGGTGGTGGCCAGATGCC 180  
 DB 41 CysLysAlaSerGlyTyrThrPheThrSerTyrTrpIleHisTrpValLysGlnArgPro 60  
 QY 181 GGGAAAGCCCTGGAGTGGATGGGATCATCTCTGGTGTACTCTGTATACACATACAGC 240  
 DB 61 GlyGlnGlyLeuValTrpIleGlyTrpIleTyrProGlyAspGlyAsnThrLysTyrAsn 80  
 QY 241 CCGTCTTCCAGGCCAGGTCAACATCTCAGCCAGCAAGTCCATCAGCAGCCGCTACTCTG 300  
 DB 81 GluLysPheLysGlyLysThrThrLeuThrAlaAspLysSerSerThrAlaTyrMet 100  
 QY 301 CAGTGGAGCAGCTTGAAGCCTCGGACACCCCATGTATTACTGTGGAGAGACCAACTG 360  
 DB 101 PheLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysThrArgGlyGly 120  
 QY 361 GGCCTCTTTGACTACTGGCCAGGAGACCTGGTCCAGCTCTCTCAGCTCCACCAAG 420  
 DB 121 TrpAlaPheAspTyrTrpGlyGlnGlyThrThrLeuThrValSerSerGluProAlaArg 140  
 QY 421 GGCCCATCGTCTTCCCTCGCTG 441  
 DB 141 GluProThrIleTyrProLeu 147

## RESULT 9

Q99L31 PRELIMINARY; PRT; 468 AA.  
 AC Q99L31;  
 DT 01-JUN-2001 (TRENBLrel. 17, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Similar to RIKEN cDNA 1810060009 gene.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003878; AAH03878.1; -.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003600; IG\_like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 3.

DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IG; 3.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00410; IG; 1.  
 DR PROSITE; PS00290; IG; MHC; UNKNOWN 1.  
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

## Alignment Scores:

Pred. No.: 1.02e-31 Length: 468  
 Score: 426.00 Matches: 82  
 Percent Similarity: 73.97% Conservative: 26  
 Best Local Similarity: 56.16% Mismatches: 36  
 Query Match: 50.35% Indels: 2  
 DB: 11 Gaps: 1

US-08-728-463B-207 (1-462) x Q99L31 (1-468)

QY 16 ATCTCGCCCTCTCTCTGCTGCTCTTCCAAAGGAGTCTGCGGAGGTGACCTGGTGGAG 75  
 Db ::  
 QY 6 ValillePhePheLeuMetAlaValValleGlyValAenSerGluValGlnLeuGln 25  
 Db ::  
 QY 76 TCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCTCTGAAGGGTTCTGGA 135  
 Db ::  
 QY 26 SerGlyAlaGluLeuValArgProGlyAlaSerVallyLeuSerCysThrAlaSerGly 45  
 Db ::  
 QY 136 TACAGCTTTACCGCTACTGGATCGCTGGTGGTGGCCAGATGCCCGGAAAGGCTGGAG 195  
 Db ::  
 QY 46 PheAnilleLysAspSerLeuMetHisTrpVallyGlnArgProGluGlnGlyLeuGlu 65  
 Db ::  
 QY 196 TGGATGGGATCATCTATCTGGTGGTCTGTACCATACATACAGCCCGTCTCTCCAGGC 255  
 Db ::  
 QY 66 TrpilleGlyTrpilleAspProGluAspGlyGluThrIlystYrAlaProLysPheGlnAsp 85  
 Db ::  
 QY 256 CAGGTCCACCTACGACGCAATCCATCAGACCCGCTACTGAGTGGAGCAGCCTG 315  
 Db ::  
 QY 86 LysAlaThrIleThrAlaAspThrSerSerAsnThrAlaYrLeuGlnLeuSerSerLeu 105  
 Db ::  
 QY 316 AAGCCTCGGACCGCCATGTATCTACTGTGCGAGACCACTG-----GGCTCTTT 369  
 Db ::  
 QY 106 ThrSerGluAspThrAlaIleTyTrCysAlaArgAsnLeuLeuTyGlyGlyTyTr 125  
 Db ::  
 QY 370 GACTACTGGGCGGAGGACCTGGTCCAGCTCTCTGCTGCTCCACCAAGGCGCCATCG 429  
 Db ::  
 QY 126 AspTyTrpGlyGlnGlyThrThrIleThrValSerSerAlalysThrThrAlaProSer 145  
 Db ::  
 QY 430 GTCTTCCCTCGGACCC 447  
 Db ::  
 QY 146 ValTyTrpLeuAlaPro 151

## RESULT 10

ID Q921K1 PRELIMINARY; PRT; 278 AA.  
 AC Q921K1  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Unknown (protein for MGC:18977).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012207; AAH12207.1;  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

## Alignment Scores:

Pred. No.: 3.82e-31 Length: 278  
 Score: 419.50 Matches: 81

Percent Similarity: 67.97% Conservative: 23  
 Best Local Similarity: 52.94% Mismatches: 44  
 Query Match: 49.59% Indels: 5  
 DB: 11 Gaps: 2

US-08-728-463B-207 (1-462) x Q921K1 (1-278)

QY 1 ATGGGGTCAACGCCCATCTCCCTCTCTGGCTGTCTTCCAAGGAGTCTGTGCCGAG 60  
 Db ::  
 Db 1 MetGlyTrpAsnCysIleLeuPheLeuValAlaThrAlaThrGlyValHisSerGln 20  
 QY 61 GTGCAGCTGCTGAGTCTGGACGACAGGTGAAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
 Db ::  
 Db 21 ValGlnLeuGlnProGlyAlaGluLeuVallyProGlyAlaSerVallyLeuSer 40  
 QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGCGCCAGATGCC 180  
 Db ::  
 Db 41 CysLysAlaSerGlyTyThrPheThrSerTyTrpMetHisTrpVallyGlnArg 60  
 QY 181 GGGAAAGCCCTGGAGTGGATCGGATCATCTATCTCTGGTACTCTGATACCATACAGC 240  
 Db ::  
 Db 61 GlyGlnGlyLeuGluTrpIleGlyAsnIleAsnProAsnSerGlyGlyThrAsnTyAsn 80  
 QY 241 CGGTCTTCCAAAGCCAGGTCAACATCTCAGCCGACAGTCCATCAGCAGCGCTACCTG 300  
 Db ::  
 Db 81 GluLysPheLysAsnLysAlaThrLeuAlaValAspLysSerSerThrValTyMet 100  
 QY 301 CAGTGGACGACCTGAGGCTCGGACACGCCCATGTATTACTGTGCGAGA----- 351  
 Db ::  
 Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyTrpCysThrArgGlyTyGly 120  
 QY 352 --GACCAACTGGGCTCTTTGACTACTGGGCGGAGGACCCCTGTACCCGCTCCCTCA 408  
 Db ::  
 Db 121 TyrAspValVal---TyrPheAspValTrpGlyAlaGlyThrThrValThrValSer 139  
 QY 409 GCCTCCCAAGGCCCATCGTCTTCCCTCCCTCGCACCC 447  
 Db ::  
 Db 140 AlalysThrThrAlaProSerValTyTrpLeuAlaPro 152

## RESULT 11

ID Q924Q0 PRELIMINARY; PRT; 143 AA.  
 AC Q924Q0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE V165-D-J-C mu protein (Fragment).  
 GN V165-D-J-C MU.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB069915; BAB63931.1;  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; ig; 1.  
 FT NON\_TER 1  
 FT NON\_TER 143  
 SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

## Alignment Scores:

Pred. No.: 4.23e-31 Length: 143  
 Score: 418.50 Matches: 80  
 Percent Similarity: 71.94% Conservative: 20  
 Best Local Similarity: 57.55% Mismatches: 34  
 Query Match: 49.47% Indels: 5



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US-08-728-463B-207 (1-462) x Q95978 (1-157)
QY 28 CTCCTGGCTGTTCTCCAGAGAGTCTGTGCGAGGTGCGAGTGTGCTGAGTGTGGAGCAG 87
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 LeuLeuAlaValAlaProGlyValHisSerGlnValGlnLeuValGlnSerGlyAlaGlu 29
QY 88 GTGAAAGACCCGGGAGTCTCTGAAGATCTCTGAAGTCTCTGAAGGTTCTGGATACAGCTTTACC 147
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 IleLysArgProGlyAlaSerValHisValHisCysLysThrSerGlyTyrValPheThr 49
QY 148 GGCCTACTGATCGGTGGTGGCGCCAGATGCCCGGGAAGCCCTGGAGTGGATGGGATC 207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 SerTyrTyrIleHisTyrValArgGlnProArgGlyGlnGlyLeuGluTyrMetGlyGly 69
QY 208 ATCTATCTCTGGTGTCTGTATACCATACATACACCGCTCTTCCAGGCCAGTCAACATC 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
70 IleGlyProGlyValGlySerThrMetCysAlaGluLysPheGlnGlyArgLeuThrMet 89
QY 268 TCAGCCGACAGTCCATCAGCACCGCTCTCTGAGTGGAGCAGCCCTGAAGGCCCTCGGAC 327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
90 ThrArgAsnThrSerThrThrValTyrMetGluLeuSerArgLeuArgPheGluAsp 109
QY 328 ACCGCCATGTATTACTGTGCAGAGAC-----CAACTGGGCTCTTTGAC---TAC 375
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
110 ThrAlaValTyrPheCysGlyArgGlyGlyArgTyrPargSerGlyAsnThrGlyHis 129
QY 376 TGGGCCAGGAGACCTGCTGTCACCGTCTCTCAGCTCCACCAAGGCCCTCGGTCTTC 435
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
130 TrpGlyGlnGlyThrProValThrValSerSerSerSerThrLysGlyProSerValPhe 149
QY 436 CCCCTGGCACCTCTCTCCAG 456
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 ProLeuAlaProCysSerArg 156

RESULT 14
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AA009851.1; -.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00041; HTH ARAC FAMILY 1; UNKNOWN_1.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Alignment Scores:
Pred. No.: 2,776-30 Length: 614
Score: 411.00 Matches: 78
Percent Similarity: 71.72% Conservative: 26
Best Local Similarity: 53.79% Mismatches: 37
Query Match: 4 Indels: 4
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x Q96GA6 (1-614)

US-08-728-463B-207 (1-462) x Q95978 (1-157)
QY 19 CTCGCCCTCTCTGCTGCTTCTCCAGAGAGTCTGTGCGAGGTGCGAGTGTGCTGAGTGT 78
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7 IleLeuPheLeuValAlaAlaAlaThrAspAlaTyrSerGlnMetGlnLeuValGlnSer 26
QY 79 GGAGCAGAGTGAAGAACCCGGGAGTCTCTGAAGATCTCTGAAGTCTCTGAAGGTTCTGATAC 138
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
27 GlyAlaGluValLysLysThrGlySerSerValLysValSerCysLysAlaSerGlyTyr 46
QY 139 AGCTTTACCGGTACTGGATCGGTGGTGGCCAGATGCCCGGGAAGCCCTGGAGTGG 198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
47 ThrPheThrTyrArgTyrLeuHisTyrValArgGlnAlaProGlyGlnAlaLeuGluTyr 66
QY 199 ATGGGGATCATCTATCTGCTGCTGCTATACCATACATACAGCCCTCTCCAGGCCAG 258
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 MetGlyTyrIleThrProPheAsnGlyAsnThrAsnTyrAlaGlnLysPheGlnAspArg 86
QY 259 GTCACATCTCAGCCAGCAAGTCCATCAGCACCGCTCTCTGAGTGGAGCAGCCCTGAAG 318
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
87 ValThrIleThrArgAspArgSerMetAsnThrAlaTyrMetGluLeuSerSerLeuArg 106
QY 319 GCCTCGGACACCGCCATCTATTACTGTGCGAGAGACCACTGGGC-----CTC 366
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
107 SerGluAspThrAlaMetTyrTyrCysAlaArgGlyTyrSerSerSerTyrAspAspAla 126
QY 367 TTTGACTACTGGGCGAGGAACTGTGTACCGTCTCTCAGCTCTCCAGCCCTCCAGGCCCA 426
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
127 PheAspIleTyrGlyGlnGlyThrMetValThrValSerSerGlySerAlaSerAlaPro 146
QY 427 TCGGTCTTCCCTCTG 441
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
147 ThrLeuPheProLeu 151

RESULT 15
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 124 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Alignment Scores:
Pred. No.: 2,346-30 Length: 124
Score: 410.50 Matches: 78
Percent Similarity: 75.59% Conservative: 18
Best Local Similarity: 61.42% Mismatches: 18
Query Match: 48.52% Indels: 13
DB: 4 Gaps: 2

US-08-728-463B-207 (1-462) x Q9UL92 (1-124)

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Search completed: June 3, 2003, 09:15:53  
Job time : 45.0121 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: June 3, 2003, 08:56:21 ; Search time 29.828 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-207  
Perfect score: 846  
Sequence: 1 ATGGGGTCAACGCCATCTCT.....CACCCCTCTCCAGAGCTT 462

Scoring table:  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-DB=A\_Geneseq\_101002\_QFMP=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CEN\_1.1.353 @runat.03062003.085613.16797 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681	80.5	474	22	AAU14177	Human novel protei
2	668.5	79.0	146	22	AAU99113	Human protein SQ
3	627	74.1	225	22	AAU75056	TRO005 Humab Happa
4	623	73.6	225	22	AAU75052	TRO005 Humab Happa
5	623	73.6	225	22	AAU75053	TRO005 Humab Happa
6	601	71.0	128	22	AAU23996	Human EST encoded
7	601	71.0	140	21	AAU56712	Amino acid sequenc
8	598	70.7	117	16	AAU66339	Human immunoglobul
9	577	68.2	121	19	AAU62798	Amino acid sequenc
10	577	68.2	240	21	AAU15128	Anti-murine CTLA-4
11	577	68.2	245	22	AAU67622	Human leukocyte an
12	574	67.8	245	22	AAU67621	Human leukocyte an
13	572.5	67.7	120	18	AAU27555	Human Ab heavy cha
14	569	67.3	117	22	AAU62966	Amino acid sequenc
15	567	67.0	245	22	AAU67623	Human leukocyte an
16	567	67.0	252	23	AAU45526	Human Blys binding
17	565	66.8	117	23	AAU15186	Digi1 antibody heav
18	562.5	66.5	139	21	AAU56727	Amino acid sequenc
19	558.5	66.0	116	23	AAU48005	Human monoclonal a
20	558.5	66.0	118	22	AAU85349	Antibody AAL 160 h
21	553.5	65.4	147	15	AAU54050	Sequence of the VH
22	553.5	65.4	147	17	AAU01528	Monoclonal antibod
23	553.5	65.4	147	18	AAU24987	Monoclonal antibod
24	551.5	65.2	249	23	AAU45301	Human Blys binding
25	530	62.6	269	23	AAU20408	Chimeric SCBP C6ML
26	530	62.6	282	23	AAU20409	Chimeric SCBP C6ML
27	530	62.6	287	23	AAU20410	Chimeric SCBP C6ML
28	530	62.6	291	23	AAU20411	Chimeric SCBP C6ML
29	530	62.6	296	23	AAU20412	Chimeric SCBP C6ML
30	528.5	62.5	142	21	AAU56708	Amino acid sequenc
31	528.5	62.5	142	21	AAU56709	Amino acid sequenc
32	527	62.3	282	23	AAU75161	Anti-interleukin-1
33	526	62.2	119	23	AAU76521	Humanised 5G1.1 VH
34	525.5	62.1	249	16	AAU77610	Humanised 5G1.1 VH
35	524	61.9	255	23	AAU20407	Chimeric SCBP C6.5
36	524	61.9	470	21	AAU90936	Humanised HFE7A de
37	524	61.9	470	23	AAU74945	Humanised anti-Fas
38	523.5	61.9	515	22	AAU52162	Humanised HMEG-1 F
39	523.5	61.9	517	22	AAU52154	Humanised HMEG-1 F
40	523.5	61.9	519	22	AAU52164	Humanised HMEG-1 F
41	523.5	61.9	519	22	AAU52165	Humanised HMEG-1 F
42	523.5	61.9	521	22	AAU52163	Humanised HMEG-1 F
43	523.5	61.9	525	22	AAU52166	Humanised HMEG-1 F
44	523.5	61.9	527	22	AAU52155	Humanised HMEG-1 F
45	523.5	61.9	529	22	AAU52168	Humanised HMEG-1 F

ALIGNMENTS

RESULT 1  
AAU14177  
ID AAU14177 standard; Protein; 474 AA.  
XX  
XX  
AC AAU14177;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human novel protein #48.  
XX  
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
OS Homo sapiens.

XX WO200155437-A2.  
 XX 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02623.  
 XX 25-JAN-2000; 2000US-0491404.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 XX WPI; 2001-451939/48.  
 XX N-PSDB; AAS22482.  
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
 XX nervous system disorders, and for regenerating bone and cartilage -  
 XX Example 4; Page 554-555; 894pp; English.  
 XX The invention relates to polynucleotides encoding novel human  
 XX proteins or their active domains. The polypeptides, polynucleotides and  
 XX antibodies raised against the polypeptides are used in a method of  
 XX treatment of a mammal and prevention of disorders caused by the aberrant  
 XX protein expression or activity. The polypeptides can be used as  
 XX molecular weight markers, food supplements, and in antibody production.  
 XX The polypeptides are used to identify compounds which bind to the  
 XX polypeptides. Polynucleotides of the invention are used as probes and  
 XX primers, for sequencing, for chromosome or gene mapping, in the  
 XX production of recombinant proteins, and in generating anti-sense DNA or  
 XX RNA and in gene therapy. Polypeptides of the invention can be used to  
 XX target drugs to a tumour, in assays to determine biological activity, to  
 XX raise antibodies/elicite an immune response, to determine quantitative  
 XX protein levels, as tissue markers, and to isolate receptors or ligands.  
 XX Polypeptides of the invention may also be useful in treating platelet  
 XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 XX ligament and/or nerve tissue, wound healing, treating burns, promoting  
 XX the proliferation, differentiation and survival of stem cells, as a  
 XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 XX fungal infection or from autoimmunity, cancer, allergy, asthma,  
 XX graft-versus-host disease, eczema, haemophilia, thrombosis,  
 XX anti-inflammatory diseases, nervous system disorders, and infection.  
 XX The present sequence represents a protein of the invention.  
 XX SQ Sequence 474 AA;  
 Alignment Scores:  
 Pred. No.: 7,27e-54 Length: 474  
 Score: 681.00 Matches: 134  
 Percent Similarity: 86.25% Conservative: 4  
 Best Local Similarity: 83.75% Mismatches: 14  
 Query Match: 80.50% Indels: 8  
 DB: 22 Gaps: 1  
 US-08-728-463b-207 (1-462) x AAU14177 (1-474)  
 QY 1 ATGGGTCAACGCCCATCTCGCCCTCTCTGCTGTCTCTCAAGGAGTCTGTCCGAG 60  
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20  
 QY 61 GTGACCTGGTTCAGTCTGGACGAGGTGAAGAGCCCGGGAGTCTCTGAAGATCTCC 120  
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerValLysIleSer 40  
 QY 121 TGTAAAGGGTCTGGATACAGCTTTACCGCTACTGATCGCTGGTGGTGGCAGATGCC 180  
 Db 41 CysLysGlySerGlyTyrSerPheSerAspTyrTrpValAlaTrpValArgGlnSerPro 60  
 QY 181 GCGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGAATCTGTATACACATACAGC 240

61 AsPLysGlyLeuAlaTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80  
 241 CGGTCTTCAAGCCAGGTCACTCTCAGCGCAAGTCAATCAGCAGCCCTACCTG 300  
 81 ProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100  
 301 CAGTGGAGCAGCTGAAGCCCTCGGACACCGCCCATGTATTACTGTGGAGAGACCACTG 360  
 101 GlnTrpSerSerLeuLysAspSerAspThrAlaMetTyrTyrCysAlaArgGlyAlaArg 120  
 361 GGCCTC-----TTTGACTACTGGGCGCAGGGAACCTGGTCT 396  
 121 GlyThrAlaProSerTyrHisTyrTyrGlyLeuAspValTrpGlyArgGlyThrSerVal 140  
 397 ACCGTCTCTCAGCCTCCACCAAGGCCCATCGTCTTCCCTCCCTGGCACCTCTCCCAAG 456  
 141 ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys 160

RESULT 2  
 AAB99113  
 ID AAB99113 standard; Protein; 146 AA.  
 AC AAB99113;  
 XX 22-AUG-2001 (first entry)  
 XX Human protein SEQ ID 8.  
 XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;  
 XX Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;  
 XX signal transduction inhibition; tissue fibrosis; atherosclerosis.  
 XX Homo sapiens.  
 XX WO200136642-A1.  
 XX 25-MAY-2001.  
 XX 17-NOV-2000; 2000WO-JP08129.  
 XX 18-NOV-1999; 99JP-0328681.  
 XX 08-NOV-2000; 2000JP-0340216.  
 XX (NTSB) JAPAN TOBACCO INC.  
 XX Sakamoto S, Kamada M;  
 XX WPI; 2001-343825/36.  
 XX N-PSDB; AAH41155.  
 XX Human monoclonal antibodies recognizing human TGF-beta II receptor,  
 XX useful for treating TGF-beta associated diseases such as tissue  
 XX fibrosis -  
 XX Claim 10; Page 100; 118pp; Japanese.  
 XX The present invention relates to novel human monoclonal antibodies. The  
 XX antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II  
 XX receptor, resulting in the inhibition of the signal transduction of human  
 XX TGF-beta into cells. The antibodies can be used for the prevention and  
 XX treatment of diseases associated with the production of TGF-beta, such as  
 XX tissue fibrosis in the lung, liver, skin, kidney or other tissues,  
 XX atherosclerosis, atopy, keloid and arthritis. The present sequence was  
 XX used in the present invention.  
 XX SQ Sequence 146 AA;  
 Alignment Scores:  
 Pred. No.: 8.39e-53 Length: 146  
 Score: 668.50 Matches: 133  
 Percent Similarity: 91.10% Conservative: 0  
 Best Local Similarity: 91.10% Mismatches: 10  
 Query Match: 79.02% Indels: 3





PN WO200125492-A1.  
 XX 12-APR-2001.  
 PD 02-OCT-2000; 2000WO-US27237.  
 PF 02-OCT-1999; 99US-0157415.  
 PR 01-DEC-1999; 99US-0453234.  
 XX (BIOS-) BIOSITE DIAGNOSTICS INC.  
 PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.  
 XX Buechler J, Valkirs G, Gray J, Lonberg N;  
 PI WPI; 2001-335567/35.  
 XX  
 DR Producing a human antibody phage display library comprising providing a  
 XX transgenic animal whose genome comprises human immunoglobulin genes and  
 XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
 PS Example 37; Page 122-123; 161pp; English.  
 XX  
 CC The present invention describes a method (M1) for producing a human  
 CC antibody phage display library (I), comprising: (1) providing a nonhuman  
 CC transgenic animal (II) whose genome comprises human immunoglobulin genes;  
 CC (2) isolating nucleic acids encoding human antibody chains (III) from  
 CC lymphatic cells; and (3) forming a library of display packages whose  
 CC members comprise a nucleic acid encoding (III) which is displayed from  
 CC the package. The method is used for producing a human antibody display  
 CC library, e.g., a Fab phage display library. The display method may be  
 CC used to screen nucleic acids encoding antibody chains obtained from  
 CC immunised nonhuman transgenic animals, and from this a population of  
 CC antibodies may be prepared. Production of a human monoclonal antibodies  
 CC display library using this method means there is no need to immunise  
 CC humans with antigens, and the difficulties faced with immortalising B  
 CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 225 AA;  
 Alignment Scores:  
 Pred. No.: 1.27e-48 Length: 225  
 Score: 623.00 Matches: 119  
 Percent Similarity: 90.98% Conservative: 2  
 Best Local Similarity: 89.47% Mismatches: 12  
 Query Match: 73.64% Indels: 0  
 DB: 22 Gaps: 0  
 US-08-728-463B-207 (1-462) x AAB75052 (1-225)  
 QY 58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCGGGGAGTCTCTGAAGATC 117  
 Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20  
 QY 118 TCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGTGGTGGCCAGATG 177  
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTyrValArgGlnMet 40  
 QY 178 CCGGGAAAGCCCTGCAGTGGATGGGATCATCTATCTCGGTGACTCTGATACCAATAC 237  
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60  
 QY 238 AGCCCTCTCTTCAAGCCAGGTTCACCATCTCAGCCGACCAAGTCCATCAGCACCGCTTAC 297  
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 QY 298 CTGCAGTGCAGCAGCTGAGCGCTCGGACACCGCATGTATTACTGTGCGAGAGACCAA 357  
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100  
 QY 358 CTGGGCGCTCTTCTACTACTTGGGGCAGGGAACCTGGTCCACGCTCTCTCAGCTCCACC 417  
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerAlaSerThr 120

QY 418 AAGGCCCATCGGTCTTCCCTGGCACCCCTCTCTCAAG 456  
 Db 121 LysGlyProSerValPheProLeuAlaProSerSerLys 133  
 RESULT 5  
 AAB75053  
 ID AAB75053 standard; Protein; 225 AA.  
 XX AAB75053;  
 XX 19-JUL-2001 (first entry)  
 XX TRO005 HuMab Happa chain protein sequence 3E3H.  
 XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
 KW human antibody phage display library; immunisation; transgenic animal.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200125492-A1.  
 XX 12-APR-2001.  
 PD 02-OCT-2000; 2000WO-US27237.  
 PF 02-OCT-1999; 99US-0157415.  
 PR 01-DEC-1999; 99US-0453234.  
 XX (BIOS-) BIOSITE DIAGNOSTICS INC.  
 PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.  
 XX Buechler J, Valkirs G, Gray J, Lonberg N;  
 PI WPI; 2001-335567/35.  
 XX  
 DR Producing a human antibody phage display library comprising providing a  
 XX transgenic animal whose genome comprises human immunoglobulin genes and  
 XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
 PS Example 37; Page 122-123; 161pp; English.  
 XX  
 CC The present invention describes a method (M1) for producing a human  
 CC antibody phage display library (I), comprising: (1) providing a nonhuman  
 CC transgenic animal (II) whose genome comprises human immunoglobulin genes;  
 CC (2) isolating nucleic acids encoding human antibody chains (III) from  
 CC lymphatic cells; and (3) forming a library of display packages whose  
 CC members comprise a nucleic acid encoding (III) which is displayed from  
 CC the package. The method is used for producing a human antibody display  
 CC library, e.g., a Fab phage display library. The display method may be  
 CC used to screen nucleic acids encoding antibody chains obtained from  
 CC immunised nonhuman transgenic animals, and from this a population of  
 CC antibodies may be prepared. Production of a human monoclonal antibodies  
 CC display library using this method means there is no need to immunise  
 CC humans with antigens, and the difficulties faced with immortalising B  
 CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 225 AA;  
 Alignment Scores:  
 Pred. No.: 1.27e-48 Length: 225  
 Score: 623.00 Matches: 119  
 Percent Similarity: 90.98% Conservative: 2  
 Best Local Similarity: 89.47% Mismatches: 12  
 Query Match: 73.64% Indels: 0  
 DB: 22 Gaps: 0  
 US-08-728-463B-207 (1-462) x AAB75053 (1-225)  
 QY 58 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCGGGGAGTCTCTGAAGATC 117  
 Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20  
 QY 118 TCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGTGGTGGCCAGATG 177  
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTyrValArgGlnMet 40  
 QY 178 CCGGGAAAGCCCTGCAGTGGATGGGATCATCTATCTCGGTGACTCTGATACCAATAC 237  
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60  
 QY 238 AGCCCTCTCTTCAAGCCAGGTTCACCATCTCAGCCGACCAAGTCCATCAGCACCGCTTAC 297  
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 QY 298 CTGCAGTGCAGCAGCTGAGCGCTCGGACACCGCATGTATTACTGTGCGAGAGACCAA 357  
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100  
 QY 358 CTGGGCGCTCTTCTACTACTTGGGGCAGGGAACCTGGTCCACGCTCTCTCAGCTCCACC 417  
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerAlaSerThr 120

Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20  
 QY 118 TCCTGTAGGCTTCGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGCGCCAGATG 177  
 Db 21 SerCysLysGlySerGlyTyrSerPheThrAsnTyrTrpIleGlyTrpValArgGlnMet 40  
 QY 178 CCGGGAAAGGCTGGAGTGGATGGGATCATCTCTGGTCACTCTGATACCATAC 237  
 Db 41 ProGlyLysGlyLeuGluTrpMetGlyPheIleTyrSerAspSerValThrArgTyr 60  
 QY 238 AGCCGCTCTTCCAGGCGAGGTCCACATCTCAGCGCAGCAAGTCCATCAGCCGCTAC 297  
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 QY 298 CTGAGTGAGAGCGCTGAAGGCTCGGACACCGCATATATCTGTCGGAGACCA 357  
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgAspGly 100  
 QY 358 CTGGGCTCTTTCACCTACTGGGGCCAGGACCTGGTCACTGCTCTCTCAGCCCTCCACC 417  
 Db 101 ProGluAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerSerAlaSerThr 120  
 QY 418 AAGGGCCCATCGCTCTTCCGCTTCCGCTGCGCACCTCTCTCCCAAG 456  
 Db 121 LysGlyProSerValPheProLeuAlaProSerSerLys 133

## RESULT 6

AAM23396  
 ID AAM23396 standard; Protein; 128 AA.  
 AC AAM23396;  
 XX

DT 12-OCT-2001 (first entry)  
 XX

DE Human EST encoded protein SEQ ID NO: 1521.  
 XX

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition.  
 XX

OS Homo sapiens.  
 XX

PN WO200154477-A2.  
 XX

PD 02-AUG-2001.  
 XX

PF 25-JAN-2001; 2001WO-US02687.  
 XX

PR 25-JAN-2000; 2000US-0491404.  
 PR

PR 17-JUL-2000; 2000US-0617746.  
 PR

PR 03-AUG-2000; 2000US-0631451.  
 PR

PR 15-SEP-2000; 2000US-0663870.  
 XX

PA (HYSE-) HYSEQ INC.  
 XX

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX

DR WPI: 2001-476164/51.  
 DR

DR N-PSDB; AAM98655.  
 XX

PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX

PS Claim 20; Page 1050; 1275pp; English.  
 XX

CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention.

SQ Sequence 128 AA;  
 XX

Alignment Scores:  
 Pred. No.: 1,19e-46 Length: 128  
 Score: 601.00 Matches: 115  
 Percent Similarity: 98.2% Conservative: 0  
 Best Local Similarity: 98.2% Mismatches: 2  
 Query Match: 71.04% Indels: 0  
 DB: 22 Gaps: 0

US-08-728-463B-207 (1-462) x AAM23396 (1-128)

QY 1 ATGGGGTCAACCGCCATCTCGCCCTCTCTGGCTGTCTTCAAGGAGTCTGTGCCGAG 60  
 Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20  
 QY 61 GTGAGCTGTGCTCAGTCTGGAGCAGAGGTGAAAAAGCCGGGAGTCTCTGAAGATCTCC 120  
 Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSer 40  
 QY 121 TGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGCGCTGCGGCTGCGCCAGATGCC 180  
 Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetPro 60  
 QY 181 GGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTGTGCTGCTCATACCATACAGC 240  
 Db 61 GlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80  
 QY 241 CCGTCTCTTCCAAAGCCAGGTCAACATCTCAGCCGACAGTCCATCAGCCGCTACCTG 300  
 Db 81 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100  
 QY 301 CAGTGGAGCAGCTCAAGCCCTCGGACACCGCCATGTATTACTGTGCGAGA 351  
 Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117

## RESULT 7

AAY56712

ID AAY56712 standard; protein; 140 AA.  
 XX

AC AAY56712;  
 XX

DT 15-FEB-2000 (first entry)  
 XX

DE Amino acid sequence of chimpanzee VH cDNA clone 41-9.  
 XX

KW Complementarity determining region; antibody; primate; immunogenicity;  
 KW Old World ape; Old World monkey; antigen-binding affinity.  
 XX

OS Pan troglodytes.  
 XX

PN WO955369-A1.  
 XX

PD 04-NOV-1999.  
 XX

PF 28-APR-1999; 99WO-US09131.  
 XX

PR 28-APR-1998; 98US-0083367.  
 XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX

PI Taylor AH;  
 XX

DR WPI: 2000-023265/02.  
 DR

DR N-PSDB; AAZ39315.  
 XX

PT Antibodies containing donor complementarity determining regions and  
 PT non-human primate acceptor frameworks, having reduced immunogenicity in  
 PT humans -  
 XX

Example 1; Page 46; 123pp; English.

PS The invention provides an antibody (Ab) comprising donor CDRs  
 CC (complementarity determining regions) derived from a non-human antigen-  
 CC specific donor antibody, and an acceptor framework from a non-human antigen-  
 CC prime. The Abs are prepared by grafting CDRs from a non-human antigen-  
 CC specific donor antibody onto homologous Old World ape or monkey acceptor  
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated  
 CC in humans (because of the close similarity between the human and primate  
 CC proteins), but retain the full antigen-binding affinity of the donor  
 CC antibody.

SQ Sequence 140 AA;

Alignment Scores:

Pred. No.: 1.2e-46 Length: 140  
 Score: 601.00 Matches: 119  
 Percent Similarity: 88.49% Conserv: 4  
 Best Local Similarity: 85.61% Mismatches: 12  
 Query Match: 71.04% Indels: 4  
 DB: 21 Gaps: 1

US-08-728-463B-207 (1-462) x AAY56712 (1-140)

QY 1 ATGGGCTCAACCGCATCTCGCCCTCTCTGCTGCTTCTCCAGGAGTGTGCCGAG 60  
 Db 2 MetGlySerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysAlaGlu 21  
 QY 61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAGATCTCC 120  
 Db 22 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSer 41  
 QY 121 TGTAGGCTTCGATCAGCTTACCGCTACTGATCGGTGGTGGCCAGATGCC 180  
 Db 42 CysLysGlySerGlyTyrSerPheThrAsnTyrTrpMetGlyTrpValCysGlnMetPro 61  
 QY 181 GGGAAAGCCCTGAGTGGATGATCATCTATCTCTGCTGCTGATCATCATACACACAGC 240  
 Db 62 GlyLysGlyProGluCysMetGlyIleIleTyrProAspSerAspThrArgTyrSer 81  
 QY 241 CCCTCCTTCCAGGCCAGGTCCATCTCAGCCGACCAAGTCCATCAGCCGCTACCTG 300  
 Db 82 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 101  
 QY 301 CAGTGGAGCAGCTTGAAGCTCGGACACCGCATGTATTACTGTCGAGA----- 351  
 Db 102 GlnTrpSerAsnLeuLysAlaSerAspThrAlaIleTyrTyrCysAlaArgCysTyrGly 121  
 QY 352 ---GACCACTGGCCCTTTGACTACTGGGCGGAGGAAACCTGTCTACCGCTCTCC 405  
 Db 122 TrpThrThrCysGluAlaPheAspIleTyrGlyGlnGlyThrMetValThrValSer 140

RESULT 8

AAW62798

ID AAR66339

XX AAR66339 standard; Protein; 117 AA.

AC AAR66339;

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PR 10-MAY-1993; 93WO-JP00603.

XX (NIBS) JAPAN TOBACCO INC.

XX Honjo T, Matsuda F;

XX WPI; 1995-006791/01.

XX N-PSDB; AAO78989.

XX DNA fragment comprising human immunoglobulin Vh genes - for the

XX production of human immunoglobulin in mammalian hosts

XX Claim 58; Page 96-97; 130pp; Japanese.

XX Protein sequences (AAR6295-51) are novel human immunoglobulin heavy

XX chain sequences encoded by novel isolated genes. The genes

XX (AAQ78939-79002) were isolated and cloned from a series of cosmid

XX constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR

XX amplification using primers AAQ78917-38. The genes are subdivided into 5

XX families of Vh genes. The fragments cover a region of 800 Kb. The DNA

XX fragments were isolated from high molecular weight DNA from human

XX placenta. The DNA was partially digested with TaqI restriction enzyme.

XX The fragments were separated by gel electrophoresis and 35-45 kb fractions

XX were collected. The fragments were ligated with ClaI-digested cosmid

XX vector pJB81. The ligation products were in vitro packed and infected

XX into E.coli 490A. The fragments were then subcloned by colony

XX hybridisation. The Vh genes and the DNA fragments encoding them are

XX useful in producing human immunoglobulin in mammalian hosts.

XX SQ Sequence 117 AA;

Alignment Scores:

Pred. No.: 2.2e-46 Length: 117  
 Score: 598.00 Matches: 114  
 Percent Similarity: 98.29% Conserv: 1  
 Best Local Similarity: 97.44% Mismatches: 2  
 Query Match: 70.69% Indels: 0  
 DB: 16 Gaps: 0

US-08-728-463B-207 (1-462) x AAR66339 (1-117)

QY 1 ATGGGCTCAACCGCATCTCGCCCTCTCTGCTGCTTCTCCAGGAGTGTGCCGAG 60

Db 1 MetGlySerThrAlaIleLeuAlaLeuLeuAlaValLeuGlnGlyValCysSerGlu 20

QY 61 GTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGAGTCTCTGAGATCTCC 120

Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIleSer 40

QY 121 TGTAGGCTTCGATCAGCTTACCGCTACTGATCGGTGGTGGCCAGATGCC 180

Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMetPro 60

QY 181 GGGAAAGCCCTGAGTGGATGATCATCTATCTCTGCTGCTGATCATCATACACACAGC 240

Db 61 GlyLysGlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyrSer 80

QY 241 CCCTCCTTCCAGGCCAGGTCCATCTCAGCCGACCAAGTCCATCAGCCGCTACCTG 300

Db 81 ProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyrLeu 100

QY 301 CAGTGGAGCAGCTTGAAGCTCGGACACCGCATGTATTACTGTCGAGA 351

Db 101 GlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 117

RESULT 9

AAW62798

ID AAR62798 standard; Peptide; 121 AA.

XX AAR62798;

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DE Amino acid sequence of a human antibody fragment.

KW Human; immunoglobulin; Ig; transgenic; non-human mammal;  
 KW inactivated endogenous Ig locus; B-cell development;  
 KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;  
 KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;  
 KW production; antibody.

XX Homo sapiens.

OS WO9824893-A2.

PN 11-JUN-1998.

XX 03-DEC-1997; 97WO-US23091.

XX 03-DEC-1996; 96US-0759620.

XX (ABGE-) ABGENIX INC.

XX Green L, Jakobovits A, Klapholz S, Kucheralapati R;  
 PI Mendez M;

XX WPI; 1998-333314/29.

XX New transgenic non-human mammals - having an inactivated  
 PT immunoglobulin locus and a near complete human immunoglobulin locus,  
 PT used for production of human antibodies

XX Disclosure; Page 74; 128pp; English.

XX AAW62793-822 represent fragments of human antibodies produced by  
 CC transgenic Xenomice, created using the method of the invention. The  
 CC specification describes a transgenic non-human mammal which has genome  
 CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)  
 CC locus, so that the mammal does not display normal B-cell development. The  
 CC modified genome also has an inserted human heavy chain Ig locus in  
 CC germline configuration, the human heavy chain Ig locus comprising a human  
 CC micro constant region and regulatory and switch sequences, human J-H  
 CC genes, human D-H genes, and human V-H genes and an inserted human kappa  
 CC light chain Ig locus in germline configuration, the human kappa light  
 CC chain Ig locus comprising a human kappa constant region, J-kappa genes,  
 CC and V-kappa genes, where the number of V-H and V-kappa genes inserted  
 CC are selected to restore normal B-cell development in the mammal. The  
 CC transgenic animals have a near complete human Ig locus, including both a  
 CC human heavy chain locus and a human kappa light chain locus. They can  
 CC be used for the production of human antibodies when exposed to  
 CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha  
 CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha  
 CC respectively.

XX SQ Sequence 121 AA;

Alignment Scores:  
 Pred. No.: 1,82e-44 Length: 121  
 Score: 577.00 Matches: 108  
 Percent Similarity: 93.16% Conservative: 1  
 Best Local Similarity: 92.31% Mismatches: 8  
 Query Match: 68.20% Indels: 0  
 DB: 19 Gaps: 0

US-08-728-463B-207 (1-462) x AAW62798 (1-121)

QY 106 TCTCTGAAGATCTCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGG 165  
 Db 1 SerLeuLysAlaSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrp 20

QY 166 GTCCGCCAGATCCCGGGAAGCCCTGGAGTGGGATCATCTATCTGGTGAATCT 225  
 Db 21 ValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSer 40

QY 226 GATACCACATACAGCCGCTCTTCAGGCCAGGTCACCATCTCAGCCGACAGTCCATC 285  
 Db 22 ValArgGlnMetProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSer 40

Db 41 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 60

QY 286 AGCACCGCTACCTGACGTGAGCAGCTGAGGCTCGACACCGCATGTATTACTGT 345  
 Db 61 SerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCys 80

QY 346 GCGAGAGACCAACTGGGCTCTTTGACTACTGGGGCCAGGGAACCTGTCACCGCTCC 405  
 Db 81 AlaArgGlnAspGlyAspSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 100

QY 406 TCAGCTCCACCAAGGGCCCATCGTCTTCCCTCCGTCACCGCTCCCAAG 456  
 Db 101 SerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArg 117

RESULT 10  
 AAY15128  
 ID AAY15128 standard; Protein; 240 AA.  
 XX AC AAY15128;  
 XX DT 07-FEB-2000 (first entry)  
 XX DE Anti-murine CTLA-4 M24 sFv.  
 XX KW Anti-murine CTLA-4 sFv; M24 sFv; single chain antibody; murine CTLA4;  
 KW membrane-associated protein; chimeric construct; extracellular domain;  
 KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;  
 KW recipient CD28; T-cell proliferation;  
 KW xenograft-specific immunosuppression.

XX OS Mus sp.  
 OS Synthetic.

XX FH Key Location/Qualifiers  
 ET Misc-difference 153  
 FT /note= "Corresponds to atc codon"

XX PN WO9957266-A2.  
 XX PD 11-NOV-1999.  
 XX PF 30-APR-1999; 99WO-GB01350.  
 XX PR 30-APR-1998; 98GB-0009280.  
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX PI Lechler IR, Dorling A;  
 XX DR WPI; 2000-038815/03.  
 XX DR N-PSDB; AAZ29000.  
 XX PT Inhibiting T-cell mediated rejection of xenotransplanted organs  
 XX PS Claim 9; Fig 11; 43pp; English.

XX The present sequence is the anti-murine CTLA-4 sFv (M24 sFv). This is a  
 CC membrane-associated protein which binds to CTLA-4. Chimeric constructs  
 CC comprising DNA sequences encoding the extracellular domain of murine  
 CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.  
 CC The anti-hCTLA4 sFv functions as a ligand binding to CTLA-4 on activated  
 CC T-cells and antagonises the co-stimulatory signal provided by the  
 CC interaction between donor B7 and recipient CD28. Cells expressing the  
 CC anti-hCTLA4 sFv failed to stimulate T-cell proliferation. This is used in  
 CC xenograft-specific immunosuppression.

XX SQ Sequence 240 AA;

Alignment Scores:  
 Pred. No.: 2,02e-44 Length: 240  
 Score: 577.00 Matches: 108  
 Percent Similarity: 94.87% Conservative: 3  
 Best Local Similarity: 92.31% Mismatches: 6



XX AAB67617-23 represent single chain antibody (scFv) fragments which  
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
 CC derived from a synthetic human combinatorial antibody library based on  
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.  
 CC The specification describes a human immunoglobulin fragments specific  
 CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
 CC studies of natural killer cell silencing as well as miscarriages.  
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
 CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
 CC fragments are useful for the preparation of a pharmaceutical for the  
 CC treatment of humans. They are also useful for HLA phenotyping.  
 XX  
 SQ Sequence 245 AA;

## Alignment Scores:

Pred. No.: 3,81e-44 Length: 245  
 Score: 574.00 Matches: 110  
 Percent Similarity: 93.22% Conservative: 0  
 Best Local Similarity: 93.22% Mismatches: 8  
 Query Match: 67.85% Indels: 0  
 DB: 22 Gaps: 0

US-08-728-463B-207 (1-462) x AAB67621 (1-245)

OY 58 GAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGAGTCTCTGAAGATC 117  
 DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20  
 OY 118 TCTGTAAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGCCAGATG 177  
 DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
 OY 178 CCGCGAAAGGCTGGAGTGGATGATCATCTATCTGGTGCATCTGATACCATAC 237  
 DB 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
 OY 238 AGCCGCTCTTCCAAAGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297  
 DB 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 OY 298 CTGCGAGTGCAGAGCTGAAGCCCTCGGACCGCCATCTATCTATCTGCGAGACCAA 357  
 DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgSerTrp 100  
 OY 358 CTGGGCTCTTTGACTACTGGGCCAGGAAACCTCGTCCAGCTCTCTCTCAGCC 411  
 DB 101 AspTyrProPheAspIleTrpGlyGlnGlyThrLeuValThrValSerSerAla 118

## RESULT 13

AAW27555  
 ID AAW27555 standard; Protein; 120 AA.

XX AAW27555;

AC AAW27555;

XX 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH5 consensus.

XX Human; antibody; preparation; library; VH5; variable region;  
 KW heavy chain; consensus.

XX Homo sapiens.

XX WO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;  
 XX WPI; 1997-179277/16.  
 DR N-PSDB; AAT87953.  
 XX Preparation of human derived antibody gene library - using synthetic  
 PT consensus sequences, and signal consensus antibody gene as universal  
 PT framework for highly diverse antibody libraries  
 XX Example 1; Fig 5F; 436pp; English.

XX The present sequence is the human antibody heavy chain  
 CC variable region synthetic sequence VH5, used in the preparation of  
 CC a human derived antibody gene library.

XX Sequence 120 AA;

## Alignment Scores:

Pred. No.: 4.69e-44 Length: 120  
 Score: 572.50 Matches: 110  
 Percent Similarity: 91.67% Conservative: 0  
 Best Local Similarity: 91.67% Mismatches: 7  
 Query Match: 67.67% Indels: 3  
 DB: 18 Gaps: 1

US-08-728-463B-207 (1-462) x AAW27555 (1-120)

OY 58 GAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCGGGAGTCTCTGAAGATC 117  
 DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20  
 OY 118 TCTGTAAAGGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGCCAGATG 177  
 DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
 OY 178 CCGCGAAAGGCTGGAGTGGATGATCATCTATCTGGTGCATCTGATACCATAC 237  
 DB 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
 OY 238 AGCCGCTCTTCCAAAGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGCCGCTAC 297  
 DB 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 OY 298 CTGCGAGTGCAGAGCTGAAGCCCTCGGACCGCCATCTATCTATCTGCGGAGA----- 351  
 DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100  
 OY 352 ---GACCAACTGGGCTCTTTGACTACTGGGGCCAGGAAACCTCGTCCAGCTCTCTCA 408  
 DB 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

## RESULT 14

AAW27555

ID AAG62966 standard; Protein; 117 AA.

XX AAG62966;

AC AAG62966;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of variable heavy chain fragment of clone G112.

XX Antibody; heavy chain; VH; amyloid protein; blood brain barrier;  
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;  
 KW transferrin receptor; neurological disease; Alzheimer's disease;  
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 82 /note= "Gln encoded by TAG"

XX





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61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
QY 298 CTGCAGTGGAGCAGCTGAAGGCTCGGACACCGCCATCTATTACTGTGCGAGAGACCAA 357  
Db |||||  
81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrCysAlaArgPheVal 100  
QY 358 CTGGGCCTCTTTGACTCTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCAGCC 411  
Db |||||  
101 ProTyrTyrMetAspAsnTrpGlyGlnGlyThrLeuValThrValSerSerAla 118

Search completed: June 3, 2003, 09:02:21  
Job time : 33.0494 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 19.6297 Seconds  
(without alignments)  
4764.744 Million cell updates/sec

Title: US-08-728-463B-207

Perfect score: 846

Sequence: 1 ATGGGCTCAACGGCCATCCT.....CACCTCTCCAGAGCTT 462

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	68.2	121	9 US-10-078-958-6	Sequence 6, Appli
2	572.5	67.7	120	9 US-10-125-687-6	Sequence 6, Appli
3	572.5	67.7	120	12 US-10-025-687-6	Sequence 6, Appli
4	567	67.0	252	9 US-09-880-748-1537	Sequence 1537, Ap

5	558.5	66.0	116	9 US-10-035-637-4	Sequence 4, Appli
6	551.5	65.2	249	9 US-09-880-748-1312	Sequence 1312, Ap
7	530	62.6	269	10 US-09-888-721-36	Sequence 36, Appl
8	530	62.6	282	10 US-09-888-721-38	Sequence 38, Appl
9	530	62.6	287	10 US-09-888-721-40	Sequence 40, Appl
10	530	62.6	291	10 US-09-888-721-44	Sequence 44, Appl
11	530	62.6	296	10 US-09-888-721-42	Sequence 42, Appl
12	527	62.3	282	9 US-09-985-442-7	Sequence 7, Appli
13	527	62.3	282	10 US-09-983-580-7	Sequence 7, Appli
14	524	61.9	255	10 US-09-888-721-34	Sequence 34, Appl
15	523.5	61.9	515	10 US-09-825-012-66	Sequence 66, Appl
16	523.5	61.9	517	10 US-09-825-012-38	Sequence 38, Appl
17	523.5	61.9	519	10 US-09-825-012-76	Sequence 76, Appl
18	523.5	61.9	519	10 US-09-825-012-80	Sequence 80, Appl
19	523.5	61.9	521	10 US-09-825-012-71	Sequence 71, Appl
20	523.5	61.9	525	10 US-09-825-012-85	Sequence 85, Appl
21	523.5	61.9	529	10 US-09-825-012-43	Sequence 43, Appl
22	523.5	61.9	529	10 US-09-825-012-95	Sequence 95, Appl
23	523.5	61.9	531	10 US-09-825-012-90	Sequence 90, Appl
24	523.5	61.9	729	10 US-09-825-012-52	Sequence 52, Appl
25	523.5	61.9	730	10 US-09-825-012-49	Sequence 49, Appl
26	523.5	61.9	731	10 US-09-825-012-46	Sequence 46, Appl
27	523.5	61.9	739	10 US-09-825-012-61	Sequence 61, Appl
28	523.5	61.9	740	10 US-09-825-012-58	Sequence 58, Appl
29	523.5	61.9	741	10 US-09-825-012-55	Sequence 55, Appl
30	523	61.8	262	9 US-09-956-086-4	Sequence 4, Appli
31	523	61.8	262	9 US-09-956-087-4	Sequence 4, Appli
32	513	60.6	98	9 US-10-194-975-45	Sequence 45, Appl
33	513	60.6	98	9 US-10-125-687-16	Sequence 16, Appl
34	513	60.6	98	12 US-10-025-687-16	Sequence 16, Appl
35	513	60.6	248	9 US-09-880-748-1995	Sequence 1995, Ap
36	509	60.2	249	9 US-09-880-748-1957	Sequence 1957, Ap
37	508.5	60.1	248	9 US-09-880-748-2088	Sequence 2088, Ap
38	506.5	59.9	248	9 US-09-880-748-1	Sequence 1, Appli
39	503	59.3	180	10 US-09-748-960-6	Sequence 6, Appli
40	502	59.3	98	10 US-09-850-165-89	Sequence 89, Appl
41	497	58.7	247	9 US-09-880-748-2103	Sequence 2103, Ap
42	490	57.9	470	10 US-09-859-053-28	Sequence 28, Appl
43	487	57.6	448	10 US-09-917-410-6	Sequence 6, Appli
44	485.5	57.4	461	9 US-09-249-011A-24	Sequence 24, Appl
45	479	56.6	470	9 US-10-020-786-9	Sequence 9, Appli

#### ALIGNMENTS

```

RESULT 1
US-10-078-958-6
; Sequence 6, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING PLURAL Vh AND Vh REGIONS AND ANTIBODIES PRODUCED THEREFROM
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-958-6
Alignment Scores: 7e-39 Length: 121
Pred. No.:

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Score: 577.00 Matches: 108  
 Percent Similarity: 93.16% Conservative: 1  
 Best Local Similarity: 92.31% Mismatches: 8  
 Query Match: 68.20% Indels: 0  
 DB: 9 Gaps: 0

US-08-728-463B-207 (1-462) x US-10-078-958-6 (1-121)

QY 106 TCCTGAAGATCTCTCTGAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGG 165  
 Db 1 SerLeuLysLeuSerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrp 20  
 QY 166 CTGCGCCAGATCGCCGGGAAAGCCCTGGAGTGGATCGGATCATCTATCTCTGGTACTCT 225  
 Db 21 ValArgGlnMetProGlyLysGlyLeuGlnTrpMetGlyLysIleLeuTyrProGlyAspSer 40  
 QY 226 GATACACATACAGCCGCTCTCAAGCCAGCTCGGACACCGCCATCTAGCCGACAACTCCATC 285  
 Db 41 AspThrArgTyrSerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIle 60  
 QY 286 AGACCGCTACTCTGAGTGGAGCAGCTCGGACACCGCCATCTATCTATCTATCTATCTGT 345  
 Db 61 SerThrAlaTyrLeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCys 80  
 QY 346 GCGAGAGACCAACTGGGCTCTTTGACTACTGGGCGCAGGAAACCCCTGGTCAACGCTCC 405  
 Db 81 AlaArgGlnAspGlyAspSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 100  
 QY 406 TCAGCTCCACCAAGGGCCCATCGGCTCTCCCTCGGACCCCTCTCCCAAG 456  
 Db 101 SerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArg 117

## RESULT 2

US-10-125-687-6  
 ; Sequence 6, Application US/10125687  
 ; Publication No. US20030054407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luo, Peter  
 ; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY  
 ; FILE REFERENCE: 26050-705  
 ; CURRENT APPLICATION NUMBER: US/10/125,687  
 ; CURRENT FILING DATE: 2002-04-17  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 120  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region  
 US-10-125-687-6

Alignment Scores:  
 Pred. No.: 1.62e-38 Length: 120  
 Score: 572.50 Matches: 110  
 Percent Similarity: 91.67% Conservative: 0  
 Best Local Similarity: 91.67% Mismatches: 7  
 Query Match: 67.67% Indels: 3  
 DB: 9 Gaps: 1

US-08-728-463B-207 (1-462) x US-10-125-687-6 (1-120)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117  
 Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlnSerLeuLysIle 20  
 QY 118 TCCTGTAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
 Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTyrValArgGlnMet 40  
 QY 278 CCCGGGAAAGGCTCGAGTGGATGGATCGGATCATCTATCTCTGGTACTCTGATACCATAC 237  
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyLysIleLeuTyrProGlyAspSerAspThrArgTyr 60

QY 238 AGCCGCTCTTCCAGGCCAGGTCCACATCTCAGCGCAGCAAGTCCATCAGACCCGCTAC 297  
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 QY 298 CTCAGTGGAGCAGCTGGAAGCCTCGGACACCGCCATGTATTACTGTCCGAGA----- 351  
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100  
 QY 352 ---GACCAACTGGGCTCTTTGACTACTGGGCGCAGGAAACCCCTGGTCAACGCTCTCTCA 408  
 Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

## RESULT 3

US-10-025-687-6  
 ; Sequence 6, Application US/10025687  
 ; Patent No. US20020142255A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luo, Peter  
 ; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY  
 ; FILE REFERENCE: 26050-705  
 ; CURRENT APPLICATION NUMBER: US/10/025,687  
 ; CURRENT FILING DATE: 2002-04-17  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 120  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Human consensus antibody heavy chain variable region  
 US-10-025-687-6

Alignment Scores:  
 Pred. No.: 1.62e-38 Length: 120  
 Score: 572.50 Matches: 110  
 Percent Similarity: 91.67% Conservative: 0  
 Best Local Similarity: 91.67% Mismatches: 7  
 Query Match: 67.67% Indels: 3  
 DB: 12 Gaps: 1

US-08-728-463B-207 (1-462) x US-10-025-687-6 (1-120)

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 Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGlnSerLeuLysIle 20  
 QY 118 TCCTGTAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
 Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
 QY 178 CCCGGGAAAGGCTCGAGTGGATGGATCGGATCATCTATCTCTGGTACTCTGATACCATAC 237  
 Db 41 ProGlyLysGlyLeuGlnTrpMetGlyLysIleLeuTyrProGlyAspSerAspThrArgTyr 60  
 QY 238 AGCCGCTCTTCCAGGCCAGGTCCACATCTCAGCGCAGCAAGTCCATCAGACCCGCTAC 297  
 Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
 QY 298 CTCAGTGGAGCAGCTGGAAGCCTCGGACACCGCCATGTATTACTGTCCGAGA----- 351  
 Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100  
 QY 352 ---GACCAACTGGGCTCTTTGACTACTGGGCGCAGGAAACCCCTGGTCAACGCTCTCTCA 408  
 Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

## RESULT 4

US-09-880-748-1537  
 ; Sequence 1537, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1537

; LENGTH: 252

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-728-463b-207 (1-462) x US-09-880-748-1537 (1-252)

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US-08-728-463b-207 (1-462) x US-09-880-748-1537 (1-252)

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Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20

QY 118 TCCTGTAGGCTTCTGGATACAGCTTTACGGCTACTGATCGGCTGGTGGCCAGATG 177

Db 21 SerCysLysGlySerGlyThrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40

QY 178 CCGGGAAGGCTGGAGTGGATCATCTATCTGGTGCATCTATCTGATACCATAC 237

Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60

QY 238 AGCCGCTCTTCCAGGCGAGTCCATCTCAGCCGACCAAGTCCATCAGCACCGCCTAC 297

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QY 298 CTGCACTGAGACGCTGAGGCTCGGACACCGCCATGTATCTGTCGGAGAGACCAA 357

Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuAsp 100

QY 358 CTGGGCTC-----TTTGACTACTGGGCGCCAGGAAACCTG 393

Db 101 TyrAspIleLeuThrGlyTyrTyrProSerGlyPheAspTyrTrpGlyGlnGlyThrMet 120

QY 394 GTACCGCTCTCTCTCA 408

Db 121 ValThrValSerSer 125

RESULT 5

US-10-035-637-4

; Sequence 4, Application US/10035637

; Publication No. US20030031667A1

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Reier, Tibor

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC

; FILE REFERENCE: MXI-166CP

; CURRENT APPLICATION NUMBER: US/10/035,637

; CURRENT FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: 09/851,614

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/203,126

; PRIOR FILING DATE: 2000-05-08

; PRIOR APPLICATION NUMBER: USSN 60/230,739

; PRIOR FILING DATE: 2000-09-07

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-035-637-4

Alignment Scores:

Pred. No.:	2,19e-37	Length:	116
Score:	558.50	Matches:	107
Percent Similarity:	93.16%	Conservative:	2
Best Local Similarity:	91.45%	Mismatches:	7
Query Match:	66.02%	Indels:	1
DB:	9	Gaps:	1

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QY 58 GAGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGGAGTCTCTGAAGATC 117

Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle 20

QY 118 TCCTGTAGGCTTCTGGATACAGCTTTACCGGCTACTGATCGGCTGGTGGCCAGATG 177

Db 21 SerCysLysGlySerGlyAspSerPheThrThrTyrTrpIleGlyTrpValArgGlnMet 40

QY 178 CCGGGAAGGCTGGAGTGGATCATCTATCTGGTGCATCTATCTGATACCATAC 237

Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrIleTyr 60

QY 238 AGCCGCTCTTCCAGGCGAGTCCATCTCAGCCGACCAAGTCCATCAGCACCGCCTAC 297

Db 61 SerProSerPheGlnGlyValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80

QY 298 CTGCACTGAGACGCTGAGGCTCGGACACCGCCATGTATCTGTCGGAGAGACCAA 357

Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysThrArgGlyAsp 100

QY 358 CTGGGCTCTTTGACTACTGGGCGCCAGGAAACCTGGTCCACCTCTCTCTCA 408

Db 101 ArgGlyVal---AspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 116

RESULT 6

US-09-880-748-1312

; Sequence 1312, Application US/09880748

; Publication No. US20030059937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1312

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-1312

Alignment Scores:		
Pred. No.:	8,296-37	Length:
Score:	551.50	Matches:
Percent Similarity:	77.33%	Conservative:
Best Local Similarity:	74.67%	Mismatches:
Query Match:	65.19%	Indels:
DB:	9	Gaps:

US-08-728-463B-207 (1-462) x US-09-880-748-1312 (1-249)

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Db	1	GINValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle	20
QY	118	TCCTCTAAGGGTTCTGGATACAGCTTTACCGGCTACTCGGATCGGCTGGGTGGCCGACATG	177
Db	21	SerCysLysGlySerGlyTyrSerPheThrLysTyrTrpIleGlyTrpValargGlnMet	40
QY	178	CCCGGGAAGCCCTGGAGTGGATGGGATCATCTATCTGTGCACCTCATACCACATAC	237
Db	41	ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAsnThrArgTyr	60
QY	238	AGCCGGTCCTTCCAGGCGCAGGTCCATCTCAGCCGACAGTCCATCAGCACCGCCTAC	297
Db	61	SerProSerPheGlnGlyGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr	80
QY	298	CTGCAGTGGAGCAGCCTGAAGGCTCGGACACCGCCATGATATCTATGTCGCGAGA	351
Db	81	LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgLeuTyr	100
QY	352	---GACCACCTG-----GGCCTCTTTGACTCTGGGGCCAGGAACCCCTG	393
Db	101	TyrAspIleLeuThrGlyTyrHisTrpAspAlaPheAspIleTrpGlyGlnGlyThrMet	120
QY	394	GTACACCGTCTCCTCAGCCTCC-----	414
Db	121	ValThrValSerSerGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlySer	140
QY	415	-----ACCAAGGCCCATCGTTC	432
Db	141	GlnSerValLeuThrGlnProProSerVal	150

## RESULT 7

US-09-888-721-36  
; Sequence 36, Application US/09888721  
; Patent No. US2002013290A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888, 721  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213, 653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine  
; OTHER INFORMATION: chimeric single chain binding polypeptide (C6ML3-9  
; OTHER INFORMATION: sfv')  
US-09-888-721-36

Alignment Scores:		
Pred. No.:	4,559-35	Length:
Score:	\$30.00	Matches:
Percent Similarity:	71.60%	Conservative:
Best Local Similarity:	65.43%	Mismatches:
Query Match:	62.65%	Indels:
DB:	10	Gaps:
		3

US-08-728-463B-207 (1-462) x US-09-888-721-36 (1-269)

58	QY	GAGGTGCAGCTGGTGCAC	TCTCGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATC	117
	Db			
1	Db	GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle	20	
	QY	TCTCTGAAGGTTCTGGATACAGCTTTACCGGCTACTCGGATCGGTCGGTGCGCCAGATG	177	
	Db			
21	Db	SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet	40	
	QY	CCCGGGAAAGCCCTGGAGTGGATGGGATCATCTATCTCTGGTGAC	237	
	Db			
41	Db	ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr	60	
	QY	AGCCCGTCTTCCAAAGCCAGGTACCATCTCAGCCGACAGTCCATCAGCACCGCCTAC	297	
	Db			
61	Db	SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr	80	
	QY	CTCAGTGGAGCAGCCCTGAAGGCTCGGACACCGCCATGTATTACTGTCCGAGAGACCA	357	
	Db			
81	Db	LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp	100	
	QY	CTGGGC	-----CTCTTTGACTACTGGGCGC	381
	Db			
101	Db	ValGlyTyrCysSerSerSerAenCysAlaLysTrpProGluTyrPheGlnHisTrpGly	120	
	QY	CAGGGAACCTTGTCACCGTCTCTCAGCCCTCC	-----	414
	Db			
121	Db	GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly	140	
	QY	415	-----ACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCC	450
	Db			
141	Db	GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal	---SerAlaAlaProGly	159
	QY	451	TCCAAG	456
	Db			
160	Db	GlnLys	161	

RESIST. T. 8

RESOL-8  
US-09-888-721-38  
; Sequence 38, Application US/09888721  
; Patent No. US20020132990A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wills, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; TITLE OF INVENTION: DELIVERY  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888,721  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine

; OTHER INFORMATION: chimeric single chain binding polypeptide  
; OTHER INFORMATION: (C6ML3-9SFV'-L1-KDEL)  
US-09-888-721-38

Alignment Scores:  
Pred. No.: 4.56e-35 Length: 282  
Score: 530.00 Matches: 106  
Percent Similarity: 71.60% Conservative: 10  
Best Local Similarity: 65.43% Mismatches: 16  
Query Match: 62.65% Indels: 30  
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-38 (1-282)

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QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAACCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGlnSerLeuLys 20
QY 118 TCCTGTAAGGGTCTGGATACAGCTTTACCGCTACTGGATCGGCTGGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTATCTGGTGCATCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 ACCCGCTCTTCAAGGCGAGTCAACATCTCAGCGCACAGTCCATCATCAGCCGCTAC 297
Db 61 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCGAGTGAGCGCTGAAGCGCTCGGACACCGCATGATATCTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTGAAGTCTGGGCG 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGAACCTGGTCACTGCTCTCCAGCCTCC-----CTCTTGAAGTCTGGGCG 414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGGCCCATCGGTCTTCCCTGGCAGCCTCC 450
Db 141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161
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## RESULT 9

US-09-888-721-40  
; Sequence 40, Application US/09888721  
; Patent No. US20020132990A1

## GENERAL INFORMATION:

; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888, 721  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 287  
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine  
; OTHER INFORMATION: chimeric single chain binding polypeptide  
; OTHER INFORMATION: (C6ML3-9SFV'-L2-KDEL)  
US-09-888-721-40

## Alignment Scores:

Pred. No.: 4.56e-35 Length: 287  
Score: 530.00 Matches: 106  
Percent Similarity: 71.60% Conservative: 10  
Best Local Similarity: 65.43% Mismatches: 16  
Query Match: 62.65% Indels: 30  
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-40 (1-287)

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QY 58 GAGGTGACGCTGGTGCAGTCTGGAGCAGAGGTGAAACCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGlnSerLeuLys 20
QY 118 TCCTGTAAGGGTCTGGATACAGCTTTACCGCTACTGGATCGGCTGGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCGGGAAGGCTGGAGTGGATGGGATCATCTATCTGGTGCATCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 ACCCGCTCTTCAAGGCGAGTCAACATCTCAGCGCACAGTCCATCATCAGCCGCTAC 297
Db 61 SerProSerPheGlnGlnValThrLysSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCGAGTGAGCGCTGAAGCGCTCGGACACCGCATGATATCTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTGAAGTCTGGGCG 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGAACCTGGTCACTGCTCTCCAGCCTCC-----CTCTTGAAGTCTGGGCG 414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGGCCCATCGGTCTTCCCTGGCAGCCTCC 450
Db 141 GlyGlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161
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## RESULT 10

US-09-888-721-44  
; Sequence 44, Application US/09888721  
; Patent No. US20020132990A1

## GENERAL INFORMATION:

; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888, 721  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 44
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6WL3-9sfv'-L2-nls)
US-09-888-721-44

Alignment Scores:
Pred. No.: 4,56e-35 Length: 291
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-44 (1-291)

QY 58 GAGGTGCAGCTGGTCACTCTGGACGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCCGGGAAAGCCCTGGAGTGGGATCATCTATCTGTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGACCCGCTAC 297
Db 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCCCTGAAAGCCCTCGGACACCGCCATGATTACTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGTGTCACCGTCTCTCAGCCTCC-----414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGTCTTCCCTCGGACCCCTCC 450
Db 141 GlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 11
US-09-888-721-42
; Sequence 42, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653

```

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; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human/murine
; OTHER INFORMATION: chimeric single chain binding polypeptide
; OTHER INFORMATION: (C6WL3-9sfv'-L2-H14)
US-09-888-721-42

Alignment Scores:
Pred. No.: 4,57e-35 Length: 296
Score: 530.00 Matches: 106
Percent Similarity: 71.60% Conservative: 10
Best Local Similarity: 65.43% Mismatches: 16
Query Match: 62.65% Indels: 30
DB: 10 Gaps: 3

US-08-728-463B-207 (1-462) x US-09-888-721-42 (1-296)

QY 58 GAGGTGCAGCTGGTCACTCTGGACGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATC 117
Db 1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLysIle 20
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40
QY 178 CCCGGGAAAGCCCTGGAGTGGGATCATCTATCTGTGACTCTGATACCATAC 237
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGACCCGCTAC 297
Db 61 SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr 80
QY 298 CTGCAGTGGAGCCCTGAAAGCCCTCGGACACCGCCATGATTACTGTCGAGAGACCAA 357
Db 81 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 100
QY 358 CTGGGC-----CTCTTTGACTACTGGGC 381
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120
QY 382 CAGGGAACCTGTGTCACCGTCTCTCAGCCTCC-----414
Db 121 GlnGlyThrLeuValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 140
QY 415 -----ACCAAGGCCCATCGTCTTCCCTCGGACCCCTCC 450
Db 141 GlyGlySerGlnSerValLeuThrGlnProProSerVal---SerAlaAlaProGly 159
QY 451 TCCAAG 456
Db 160 GlnLys 161

RESULT 12
US-09-985-442-7
; Sequence 7, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Ac
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19

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; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFv  
US-09-985-442-7

Alignment Scores:  
Pred. No.: 7,97e-35 Length: 282  
Score: 527.00 Matches: 100  
Percent Similarity: 77.40% Conservativeness: 13  
Best Local Similarity: 68.49% Mismatches: 21  
Query Match: 62.29% Indels: 12  
DB: 9 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-985-442-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117  
Db 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149  
QY 118 TCCTGTAAGGGTCTCGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
Db 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPileAlaTrpValArgGlnMet 169  
QY 178 CCGGGAAGGCTGAGTGGATCGGATCATCTACCGGCTACTGGATCGGCTGGTGGCCAGATG 237  
Db 170 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 189  
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297  
Db 190 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlnTyrPheGlnHisTrpGly 249  
QY 382 CAGGGAACCTGGTCCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441  
Db 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269

US-08-728-463B-207 (1-462) x US-09-985-442-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117  
Db 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149  
QY 118 TCCTGTAAGGGTCTCGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
Db 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPileAlaTrpValArgGlnMet 169  
QY 178 CCGGGAAGGCTGAGTGGATCGGATCATCTACCGGCTACTGGATCGGCTGGTGGCCAGATG 237  
Db 170 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 189  
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297  
Db 190 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlnTyrPheGlnHisTrpGly 249  
QY 382 CAGGGAACCTGGTCCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441  
Db 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269

QY 442 GCACCCCTCTCCCAAGAG 459  
Db 270 SerLysLysLysLysLysLys 275

RESULT 13  
US-09-983-580-7  
; Sequence 7, Application US/09983580  
; Patent No. US20020151061A1  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David R..  
; APPLICANT: Wang, Maoliang  
; APPLICANT: Whitlow, Marc D.  
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid  
; FILE REFERENCE: 0977.2300002  
; CURRENT APPLICATION NUMBER: US/09/983,580  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 09/420,592  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/104,949  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7

US-08-728-463B-207 (1-462) x US-09-983-580-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117  
Db 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149  
QY 118 TCCTGTAAGGGTCTCGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
Db 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPileAlaTrpValArgGlnMet 169  
QY 178 CCGGGAAGGCTGAGTGGATCGGATCATCTACCGGCTACTGGATCGGCTGGTGGCCAGATG 237  
Db 170 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 189  
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297  
Db 190 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlnTyrPheGlnHisTrpGly 249  
QY 382 CAGGGAACCTGGTCCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441  
Db 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269

QY 442 GCACCCCTCTCCCAAGAG 459  
Db 270 SerLysLysLysLysLysLys 275

RESULT 14  
US-09-888-721-34  
; Sequence 34, Application US/09888721  
; Patent No. US20020132990A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888,721  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

US-08-728-463B-207 (1-462) x US-09-983-580-7 (1-282)

QY 58 GAGGTGACGTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGGAGTCTCTGAAGATC 117  
Db 130 GlnValGlnLeuLeuGlnSerGlyAlaGlnLeuLysLysProGlyGlnSerLeuLysIle 149  
QY 118 TCCTGTAAGGGTCTCGGATACAGCTTTACCGGCTACTGGATCGGCTGGTGGCCAGATG 177  
Db 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTriPileAlaTrpValArgGlnMet 169  
QY 178 CCGGGAAGGCTGAGTGGATCGGATCATCTACCGGCTACTGGATCGGCTGGTGGCCAGATG 237  
Db 170 ProGlyLysGlyLeuGlnTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 189  
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCCGCTAC 297  
Db 190 SerProSerPheGlnGlnValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGCACTGAGCAGCTGAAGGCTCGGACACCGCATCTATTACTGTCCGAGAGACCAA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTGACTACTGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGlnTyrPheGlnHisTrpGly 249  
QY 382 CAGGGAACCTGGTCCACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCCCTG 441  
Db 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269

QY 442 GCACCCCTCTCCCAAGAG 459  
Db 270 SerLysLysLysLysLysLys 275

RESULT 14  
US-09-888-721-34  
; Sequence 34, Application US/09888721  
; Patent No. US20020132990A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Wils, Pierre  
; APPLICANT: Zhu, Quan  
; APPLICANT: Laurent, Olivier  
; APPLICANT: Marasco, Wayne A.  
; APPLICANT: Scherman, Daniel  
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID  
; FILE REFERENCE: 23611-A USA  
; CURRENT APPLICATION NUMBER: US/09/888,721  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: 60/213,653  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Artificial Sequence



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 10.5159 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

Title: US-08-728-463B-207  
Perfect score: 846  
Sequence: 1 ATGGGGTCAACCGCATCTT.....CACCTCTCTCAAGAGCTT 462

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xip  
-Q=/cgn2\_1/USPTO spool/US08728463/runat\_03062003\_085615\_16867/app query.fasta\_1.3690  
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CEN 1 1 97 @runat\_03062003\_085615\_16867 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5A COMB.pcp:\*  
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3: /cgn2\_6/prodata/1/aa/6A COMB.pcp:\*  
4: /cgn2\_6/prodata/1/aa/6B COMB.pcp:\*  
5: /cgn2\_6/prodata/1/aa/PCTUS COMB.pcp:\*  
6: /cgn2\_6/prodata/1/aa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	598	70.7	117	3	US-08-545-809A-133
2	576	68.1	119	4	US-09-025-769B-26
3	572.5	67.7	120	4	US-09-025-769B-40
4	572.5	67.7	120	4	US-09-025-769B-67
5	553.5	65.4	147	1	US-08-259-372A-8
6	553.5	65.4	147	1	US-08-468-671-8
7	527	62.3	282	4	US-09-420-592A-7
8	524	61.9	258	2	US-08-665-202-5
9	523	61.8	262	4	US-09-069-821-4
10	520	61.5	129	2	US-08-665-202-32
11	513	60.6	98	2	US-08-665-202-33
12	508	60.0	98	1	US-08-478-039-81

13	508	60.0	98	1	US-08-476-349A-81
14	503	59.5	125	2	US-08-665-202-44
15	501	59.2	125	2	US-08-665-202-53
16	501	59.2	125	2	US-08-665-202-54
17	501	59.2	125	2	US-08-665-202-59
18	500	59.1	222	1	US-08-458-516-22
19	500	59.1	235	1	US-08-458-516-23
20	500	59.1	449	1	US-08-458-516-13
21	499	59.0	125	2	US-08-665-202-45
22	499	59.0	125	2	US-08-665-202-46
23	499	59.0	125	2	US-08-665-202-48
24	499	59.0	125	2	US-08-665-202-55
25	497	58.7	125	2	US-08-665-202-58
26	496	58.6	125	2	US-08-665-202-51
27	496	58.6	125	2	US-08-665-202-52
28	496	58.6	125	2	US-08-665-202-56
29	492	58.2	125	2	US-08-665-202-50
30	492	58.2	125	2	US-08-665-202-57
31	489	57.8	98	2	US-08-428-197-17
32	489	57.8	98	5	PCT-US93-10555-17
33	488	57.7	125	2	US-08-665-202-49
34	487.5	57.6	122	4	US-08-983-607-30
35	483	57.1	125	2	US-08-665-202-47
36	483	57.1	249	4	US-08-918-148-74
37	477	56.4	476	2	US-08-378-939-10
38	468.5	55.4	467	2	US-07-916-098A-45
39	462	54.6	468	4	US-09-485-737B-67
40	462	54.6	711	4	US-09-485-737B-90
41	461.5	54.6	253	3	US-09-027-449-52
42	461.5	54.6	253	3	US-08-804-444A-52
43	461.5	54.6	253	4	US-09-026-985-52
44	461.5	54.6	253	4	US-09-121-952A-52
45	461.5	54.6	253	4	US-09-234-340A-52

ALIGNMENTS

RESULT 1  
US-08-545-809A-133  
; Sequence 133, Application US/08545809A  
; Patent No. 6096878  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; APPLICANT: Matsuda, Fumihiro  
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
; NUMBER OF SEQUENCES: 145  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/545,809A  
; FILING DATE: 27-MAR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP93/00603  
; FILING DATE: 10-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 06501/004001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154



;; ZIP: 10021  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769B  
;; FILING DATE: 18-FEB-1998  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 40:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 120 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-025-769B-40

Alignment Scores:  
Pred. No.: Length: 120  
Score: 572.50 Matches: 110  
Percent Similarity: 91.67% Conservative: 0  
Best Local Similarity: 91.67% Mismatches: 7  
Query Match: 67.67% Indels: 3  
DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-025-769B-40 (1-120)

QY 58 GAGGTGACGCTGGTGGATCGGATCACTATCTCTGGTGGAGTCTCTGAAGATC 117  
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLys 20  
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGCTGGCGCAGATG 177  
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
QY 178 CCGGGAAGGCTGGAGTGGATCGGATCACTATCTCTGGTGGAGTCTCTGAAGATC 237  
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
QY 238 AGCCCGTCTCTCAAGGCGAGTCACTACCATCTCAGCCGACAAAGTCCATCAGACCCGCTAC 297  
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
QY 298 CTGCACTGAGAGCTGAAGGCTCGGACCGGATGATATATCTGTCGAGA----- 351  
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100  
QY 352 ---GACCAACTGGGCTCTTTGACTCTGGGCGGGAACCTGGTCAACCGTCTCTCA 408  
Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

## RESULT 4

US-09-025-769B-67  
; Sequence 67, Application US/09025769B  
; Patent No. 630064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas

;; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
;; NUMBER OF SEQUENCES: 373  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
;; STREET: 1251 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10021  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/025,769B  
;; FILING DATE: 18-FEB-1998  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95 11 3021.0  
;; FILING DATE: 18-AUG-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: James F. Haley, Jr., Esq.  
;; REGISTRATION NUMBER: 27,794  
;; REFERENCE/DOCKET NUMBER: MORPHO/5  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)596-9000  
;; TELEFAX: (212)596-9090  
;; INFORMATION FOR SEQ ID NO: 67:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 120 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-025-769B-67

Alignment Scores:  
Pred. No.: Length: 120  
Score: 572.50 Matches: 110  
Percent Similarity: 91.67% Conservative: 0  
Best Local Similarity: 91.67% Mismatches: 7  
Query Match: 67.67% Indels: 3  
DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-025-769B-67 (1-120)

QY 58 GAGGTGACGCTGGTGGATCGGATCACTATCTCTGGTGGAGTCTCTGAAGATC 117  
Db 1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyGluSerLeuLys 20  
QY 118 TCCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGATCGGCTGGCGCAGATG 177  
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
QY 178 CCGGGAAGGCTGGAGTGGATCGGATCACTATCTCTGGTGGAGTCTCTGAAGATC 237  
Db 41 ProGlyLysGlyLeuGluTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
QY 238 AGCCCGTCTCTCAAGGCGAGTCACTACCATCTCAGCCGACAAAGTCCATCAGACCCGCTAC 297  
Db 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
QY 298 CTGCACTGAGAGCTGAAGGCTCGGACCGGATGATATATCTGTCGAGA----- 351  
Db 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgTrpGly 100  
QY 352 ---GACCAACTGGGCTCTTTGACTCTGGGCGGGAACCTGGTCAACCGTCTCTCA 408  
Db 101 GlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 120

## RESULT 5

US-08-259-372A-8  
; Sequence 8, Application US/08259372A  
; Patent No. 5565354

GENERAL INFORMATION:  
APPLICANT: Ostberg, Lars G.  
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,372A  
FILING DATE: 14-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-259-372A-8

Alignment Scores:  
Pred. No.: 1,09e-46 Length: 147  
Score: 553.50 Matches: 109  
Percent Similarity: 78.23% Conservative: 6  
Best Local Similarity: 74.15% Mismatches: 21  
Query Match: 65.43% Indels: 11  
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-259-372A-8 (1-147)

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Db 1 MetGlySerThrAlaIleLeuGlyLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20  
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QY 61 GTGCAGCTGGTCACTGTGACACAGAGTGAAGACCCGGGAGTCTCTGAAGATCTCC 120  
|||||  
Db 21 ValGlnLeuValGlnSerGlyAlaGluValIleGlySerProGlyGluSerLeuArgIleSer 40  
|||||  
QY 12\* TGTAAAGGTTCTGGATACAGCTTTTACCGGCTACTGGATCGGCTGGTGGCCAGATGCC 180  
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Db 41 CysLySGlySerGlyTyrSerPheThrSerTyrTTPileSerTTPValArgInMetPro 60  
|||||  
QY 181 GGGAAGGCTGGAGTGGATGGGATCATCTATCTCTGGTGGTACTCTGATACCATACAGC 240  
|||||  
Db 61 GlyLySGlyLeuGlnIlePheMetGlyArgLeuAppProSerAlaSerSerAlaIlePheSer 80  
|||||  
QY 241 CCTCTCTTCAAGGCCAGGTCCACCATCTCAGCCGACCAAGTCCATCAGCAGCCGCTTACCTG 300  
|||||  
Db 81 ProSerLeuGlnGlyHisValThrIleSerValAspLysSerMetArgThrAlaTyrVal 100  
|||||  
QY 301 CAGTGGAGCAGCTGAAGCCCTCGGACACCCGCTATCTATCTGTGCGAGAGACCAA--- 357  
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Db 101 GlnTrpArgSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisValArg 120  
|||||  
QY 358 -----CTGGGCTCTTTGACTCTCTGACTCTGGGGCAGGGA 387  
|||||  
Db 121 GluLysSerMetValGlnGlyValIleIleLysAlaPheAspIleTTPGlyGlnGly 140  
|||||  
QY 388 ACCCTGGTCAACGCTCTCTCTCA 408  
|||||  
Db 141 ThrMetValThrValSerSer 147

## RESULT 6

US-08-468-671-8  
Sequence 8, Application US/08468671  
Patent No. 5648077  
GENERAL INFORMATION:  
APPLICANT: Ostberg, Lars G.  
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,671  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/259,372  
FILING DATE: 14-JUN-1994  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/192,754  
FILING DATE: 11-MAY-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-671-8

Alignment Scores:  
Pred. No.: 1,09e-46 Length: 147  
Score: 553.50 Matches: 109  
Percent Similarity: 78.23% Conservations: 6  
Best Local Similarity: 74.15% Mismatches: 21  
Query Match: 65.43% Indels: 11  
DB: 1 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-468-671-8 (1-147)

QY 1 ATGGGGTCAACCGGCATCTCCCTCTCTCTGGTGTCTTCCAAAGGAGTCTGTGCCGAG 60  
Db 1 MetGlySerThrAlaIleLeuGlyLeuLeuAlaValLeuGlnGlyValCysAlaGlu 20  
QY 61 GTCCAGCTGGTCCAGTCTGGACGAGGTGAAAGCCCGGGAGTCTCTGAAGATCTCC 120  
Db 21 ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuArgIleSer 40  
QY 121 TCTAAGGGTCTGGATACAGCTTTACCGGCTACTGTGATCGGCTGGTGGCCAGATGCC 180  
Db 41 CysLysGlySerGlyTyrSerPheThrSerTyrTrpIleSerTyrPvalArgGlnMetPro 60  
QY 181 GGGAAAGGCTCGAGTGGATGGGATCATCTCTGGTGTGATCTGTATACCATACATACAGC 240  
Db 61 GlyLysGlyLeuGluTrpMetGlyArgLeuAspProSerAlaSerSerAlaIlePheSer 80  
QY 241 CGTCTCTCCAGGCGAGTCCATCTCAGCGGACAGTCCATCAGCACCGCTACCTG 300  
Db 81 ProSerLeuGlnGlyHisValThrIleSerValAspLysSerMetArgThrAlaTyrVal 100  
QY 301 CAGTGAGCAGCTGAAGCCCTCGGACACCGCATGTATTACTGTGCGAGAGACCAA--- 357  
Db 101 GlnTrpArgSerLeuLysAlaSerThrAlaMetTyrTyrCysAlaArgHisValArg 120  
QY 358 -----CTGGGCTCTTTGACTTGTGACTTGTGGGCGCAGGGA 387  
Db 121 GluLysSerMetValGlnGlyValIleIleLysAspAlaPheAspIleTrpGlyGlnGly 140  
QY 388 ACCCTGGTCCAGTCTCTCTCA 408  
Db 141 ThrMetValThrValSerSer 147

RESULT 7

US-09-420-592A-7  
Sequence 7, Application US/09420592A  
Patent No. 6333396  
GENERAL INFORMATION:  
APPLICANT: Filpula, David R.  
APPLICANT: Wang, Maoliang  
APPLICANT: Whitlow, Marc D.  
TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids  
FILE REFERENCE: 0977.2300001  
CURRENT APPLICATION NUMBER: US/09/420,592A  
CURRENT FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/104,949  
PRIOR FILING DATE: 1998-10-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 7  
LENGTH: 282  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sFV  
US-09-420-592A-7

Alignment Scores:  
Pred. No.: 5,29e-44 Length: 282  
Score: 527.00 Matches: 100  
Percent Similarity: 77.40% Conservations: 13  
Best Local Similarity: 68.49% Mismatches: 21  
Query Match: 62.29% Indels: 12  
DB: 4 Gaps: 1

US-08-728-463B-207 (1-462) x US-09-420-592A-7 (1-282)

QY 58 GAGTGCAGCTGCTGCTCAGTCTGACGACAGGTGAAAGCCCGGGAGTCTCTGAAGATC 117  
Db 130 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 149  
QY 118 TCCTGTAAGGGTCTGGATACAGCTTTACCGGCTACTGTGATCGGCTGGTGGCCAGATG 177  
Db 150 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 169  
QY 178 CCCGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTGTGACTCTGTATACCATAC 237  
Db 170 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 189  
QY 238 AGCCCGTCTTCCAAAGCCAGGTCCATCTCAGCCGACCAAGTCCATCAGCACCGCTAC 297  
Db 190 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGACGTGAGCAGCTGAAGCCCTCGACACCGCATGTATTACTGTCCGAGAGACCA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTTGACTTGTGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 249  
QY 382 CAGGAAACCTGTGTGCTCAGCTCTCTCAGCTCCACAGAGGCGCCATCGGTCTTCCCGCTG 441  
Db 250 GlnGlyThrLeuValThrValSerSerLysLysLysLysLysLysValThrVal 269  
QY 442 GCACCTCTCCNAGAAG 459  
Db 270 SerLysLysLysLysLys 275

RESULT 8

US-08-665-202-5  
Sequence 5, Application US/08665202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238





Db 190 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaTyr 209  
QY 298 CTGAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGTATATCTGCGAGAGACCAA 357  
Db 210 LeuGlnTrpSerSerLeuLysProSerAspAlaValTyrPheCysAlaArgHisAsp 229  
QY 358 CTGGGC-----CTCTTTGACTACTGGGGC 381  
Db 230 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 249  
QY 382 CAGGGAACCTGGTCAACCTCTCCCTCAGCCCTCAC 417  
Db 250 GlnGlyThrLeuValThrValSerSerAsnLysThr 261

RESULT 10  
US-08-665-202-32  
; Sequence 32, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 129 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-665-202-32

Alignment Scores:  
Pred. No.: 2,08e-43 Length: 129  
Score: 520.00 Matches: 97  
Percent Similarity: 83.72% Conservative: 11  
Best Local Similarity: 75.19% Mismatches: 9  
Query Match: 61.47% Indels: 12  
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-665-202-32 (1-129)  
QY 58 GAGGTGCAGCTGGTGCAGTCTGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAGATC 117

Db 1 GlnValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle 20  
QY 118 TCCTTAAGGGTCTTGATACAGCTTTTACCGGCTACTGGATCGGTGGTGGCCAGATG 177  
Db 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleAlaTrpValArgGlnMet 40  
QY 178 CCCGGAAAGCGCTGGAGTGGATGGGATCATCTATCTCTGGTGACTGTGATACCATAC 237  
Db 41 ProGlyLysGlyLeuGluTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60  
QY 238 AGCCCGTCTCTTCCAAAGGCCAGGTCAACCATCTCAGCCGCAAGTCCATCAGCACCGCTAC 297  
Db 61 SerProSerPheGlnGlyValThrIleSerValAspLysSerValSerThrAlaLys 80  
QY 298 CTGAGTGGAGCAGCTGAAGCCCTCGGACACCGCATGTATATCTGCGAGAGACCAA 357  
Db 81 LeuGlnTrpSerSerLeuLysProSerAspAlaValTyrPheCysAlaArgHisAsp 100  
QY 358 CTGGGC-----CTCTTTGACTACTGGGGC 381  
Db 101 ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120  
QY 382 CAGGGAACCTGGTCAACCTCTCCCTCA 408  
Db 121 GlnGlyThrLeuValThrValSerSer 129

RESULT 11  
US-08-665-202-33  
; Sequence 33, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061410  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-665-202-33

## Alignment Scores:

Pred. No.: 9,4e-43 Length: 98  
Score: 513.00 Matches: 96  
Percent Similarity: 97.96% Conservative: 0  
Best Local Similarity: 97.96% Mismatches: 2  
Query Match: 60.64% Indels: 0  
DB: 2 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-665-202-33 (1-98)

QY 58 GAGTGCAGCTGTGAGTCTGAGCAGAGTGAAGAGCCCGGGAGTCTCTGAAGATC 117  
DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysile 20  
QY 118 TCCTGAAGGTTCTCGATACAGCTTTACCGCTACTGATCGCTGGTGGTGGCCAGATG 177  
DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
QY 178 CCGGGAAGGCTGAGTGGATGGGATCATCTATCTGTGACTCTGTATACCATAC 237  
DB 41 ProGlyLysGlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
QY 238 AGCCGCTCTCTCAAGGCGAGTCCACCATCTCAGCGGCAAGTCCATCAGCAGCCCTAC 297  
DB 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
QY 298 CTGCAGTGCAGAGCTGAAGGCTCGACACCGCCATGTATTACTGTGCGAGA 351  
DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 98

## RESULT 12

US-08-478-039-81  
Sequence 81, Application US/08478039  
Patent No. 5681722

## GENERAL INFORMATION:

APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabil  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,039  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 81:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: VHS consensus

US-08-478-039-81

Alignment Scores:

Pred. No.: 2,92e-42 Length: 98  
Score: 508.00 Matches: 95  
Percent Similarity: 96.94% Conservative: 0  
Best Local Similarity: 96.94% Mismatches: 3  
Query Match: 60.05% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-478-039-81 (1-98)

QY 58 GAGTGCAGCTGTGAGTCTGAGCAGAGTGAAGAGCCCGGGAGTCTCTGAAGATC 117  
DB 1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysile 20  
QY 118 TCCTGAAGGTTCTCGATACAGCTTTACCGCTACTGATCGCTGGTGGTGGCCAGATG 177  
DB 21 SerCysLysGlySerGlyTyrSerPheThrSerTyrTrpIleGlyTrpValArgGlnMet 40  
QY 178 CCGGGAAGGCTGAGTGGATGGGATCATCTATCTGTGACTCTGTATACCATAC 237  
DB 41 ProGlyLysGlyLeuGlnTrpMetGlyIleIleTyrProGlyAspSerAspThrArgTyr 60  
QY 238 AGCCGCTCTCTCAAGGCGAGTCCACCATCTCAGCGGCAAGTCCATCAGCAGCCCTAC 297  
DB 61 SerProSerPheGlnGlnValThrIleSerAlaAspLysSerIleSerThrAlaTyr 80  
QY 298 CTGCAGTGCAGAGCTGAAGGCTCGACACCGCCATGTATTACTGTGCGAGA 351  
DB 81 LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArg 98

## RESULT 13

US-08-476-349A-81

Sequence 81, Application US/08476349A

Patent No. 5750105

## GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/379,072  
;; FILING DATE: 25-JAN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/912,292  
;; FILING DATE: 10-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/856,281  
;; FILING DATE: 23-MAR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/735,064  
;; FILING DATE: 25-JUL-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Teskin Esq., Robin L.  
;; REGISTRATION NUMBER: 35,030  
;; REFERENCE/DOCKET NUMBER: 012712-161  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-836-6620  
;; TELEFAX: 703-836-2021  
;; INFORMATION FOR SEQ ID NO: 81:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 98 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT: VH5 consensus  
US-08-476-349A-81

Alignment Scores:  
Pred. No.: 2,92e-42 Length: 98  
Score: 508.00 Matches: 95  
Percent Similarity: 96.94% Conservative: 0  
Best Local Similarity: 96.94% Mismatches: 3  
Query Match: 60.05% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-207 (1-462) x US-08-476-349A-81 (1-98)

QY	58	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC	117
DB	1	GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyGluSerLeuLysIle	20
QY	118	TCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCCAGATG	177
DB	21	SerCysLysGlySerGlyTyrSerPheThrSeryrTrpIleGlyTrpValargGlnMet	40
QY	178	CCCGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC	237
DB	41	ProGlyLysGlyLeuGluTrpMetGlyIlelleTyrProGlyAspSerAspThrargTyr	60
QY	238	ACCCGTCCTTCAGAGCCAGGTACCATCTACGCGCAAGTCATCATGACGACCGCTAC	297
DB	61	SerProSerPheGlnGlyHisValThrIleSerAlaAspLysSerIleSerThrAlaTyr	80
QY	298	CTGCAGTGCAGGCTGAAGGCTCGGACACCGCCATCTATTACTGTGCGGAGA	351
DB	81	LeuGlnTrpSerSerLeuLysAlaSerAspThrAlaMetCtyrTyrCysAlaarg	98

RESULT 14

US-08-665-202-44  
; Sequence 44, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/665,202  
;; FILING DATE: 13-JUN-1996  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/000,238  
;; FILING DATE: 14-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/000,250  
;; FILING DATE: 15-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hunter, Tom  
;; REGISTRATION NUMBER: 38,498  
;; REFERENCE/DOCKET NUMBER: 02307E-061410  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 125 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-665-202-44

Alignment Scores:  
Pred. No.: 9,7e-42 Length: 125  
Score: 503.00 Matches: 93  
Percent Similarity: 83.20% Conservative: 11  
Best Local Similarity: 74.40% Mismatches: 9  
Query Match: 59.46% Indels: 12  
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-665-202-44 (1-125)

QY	58	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAGCCCGGGAGTCTCTGAAGATC	117
DB	1	GluValGlnLeuLeuGlnSerGlyAlaGluLeuLysLysProGlyGluSerLeuLysIle	20
QY	118	TCTGTAAAGGTTCTGGATACAGCTTTACCGGCTACTGGATCGGCTGGGTGCCAGATG	177
DB	21	SerCysLysGlySerGlyTyrSerPheThrSeryrTrpIleAlaTrpValargGlnMet	40
QY	178	CCCGGAAAGGCTGGAGTGGATGGGATCATCTATCTGTGACTCTGATACCATAC	237
DB	41	ProGlyLysGlyLeuGluTrpMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr	60
QY	238	ACCCGTCCTTCAGAGCCAGGTACCATCTACGCGCAAGTCATCATGACGACCGCTAC	297
DB	61	SerProSerPheGlnGlyGlnValThrIleSerValAspLysSerValSerThrAlaTyr	80
QY	298	CTGCAGTGCAGGCTGAAGGCTCGGACACCGCATGTATTACTGTGCGGAGACCAA	357
DB	81	LeuGlnTrpSerSerLeuLysProSerAspSerAlaValTyrPheCysAlaargHisAsp	100
QY	358	CTGGGC-----CTCTTGTACTACTGGGC	381
DB	101	ValGlyTyrCysSerSerSerAsnCysAlaLysTrpProGluTyrPheGlnHisTrpGly	120
QY	382	CAGGAAACCTGGTC	396

Db 121 GlnGlyThrLeuVal 125

RESULT 15  
US-08-665-202-53  
; Sequence 53, Application US/08665202  
; Patent No. 5977322  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D.  
; APPLICANT: Schier, Robert  
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
; TITLE OF INVENTION: Tumor Antigens  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,202  
; FILING DATE: 13-JUN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,238  
; FILING DATE: 14-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,250  
; FILING DATE: 15-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 02307E-061410  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-665-202-53

Alignment Scores:  
Pred. No.: 1.53e-41 Length: 125  
Score: 501.00 Matches: 94  
Percent Similarity: 82.40% Conservative: 9  
Best Local Similarity: 75.20% Mismatches: 10  
Query Match: 59.22% Indels: 12  
DB: 2 Gaps: 1

US-08-728-463B-207 (1-462) x US-08-665-202-53 (1-125)

QY 58 GAGTGCAGCTGCTGAGTCTGGAGCAGAGTGAAAGCCCGGGAGTCTCTGAAGATC 117  
Db 1 GlnValGlnLeuValGlnSerGlyGlyGluMetLysLysProGlyGluSerLeuLysile 20  
QY 118 TCCTGTAAAGGGTCTCGATACAGCTTTACCGCTACTCGATCGGCTGGTGGCCAGATG 177  
Db 21 SerCysLysGlyLeuGlyTyrAspPheSerThrTyrTrpIlealaTrpValArgGlnMet 40  
QY 178 CCGGGAAAGGCTGGATGGATCGGATCATCTATCTGTGACTCTGTATACCATAC 237  
Db 41 ProGlyLysGlyLeuGlyTyrMetGlyLeuIleTyrProGlyAspSerAspThrLysTyr 60  
QY 248 AGCCCGTCTCTCCAGGCGAGTCCACCATCTCAGCGAGACAGTCCATCAGCAGCCGCTAC 297

Db 61 SerProSerPheGlnGlyGlnValThrIleSerAlaAspGluSerIleSerThrAlaTyr 80  
QY 298 CTGCAGTGGAGCAGCCTGAGGCTCGGACACCGCCATGTATTACTGTCCGAGAGACCAA 357  
Db 81 LeuGluTrpSerSerLeuLysAlaSerAspThrAlaMetTyrTyrCysAlaArgHisApp 100  
QY 358 CTGGGC-----CTCTTTGACTACTGGGGC 381  
Db 101 ValGlyTyrCysSerSerSerAanCysAlaLysTrpProGluTyrPheGlnHisTrpGly 120  
QY 382 CAGGGAACCTGGTC 396  
Db 121 GlnGlyThrLeuVal 125

Search completed: June 3, 2003, 09:47:28  
Job time : 13.5159 secs





A:Molecule type: mRNA

A:Residues: 1-132 <KLE>

A:Cross-references: EMBL:X72444

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2,7e-44	Length:	132
Score:	577.00	Matches:	110
Percent Similarity:	92.42%	Conservative:	12
Best Local Similarity:	83.33%	Mismatches:	10
Query Match:	72.95%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-208 (1-439) x S40334 (1-132)

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QY 4 GACATGGAGTTCCTCCGCTTCAGCTCCTGGGCTCTGCTGCTCTGTTTCCAGGTGCCAGA 63
Db 1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArg 20

QY 64 TGTGATCCAGATGACCCAGTCTCCATCCTCACTGCTGTGATCTGTAGGAGACAGATC 123
Db 21 CysAspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerIleGlyAspArgVal 40

QY 124 ACATCACTTGTCCGGCAGTCAGGTATAGCAGCTGTTAGCTGTTAGCTATCAGCAGAAA 183
Db 41 ThrIleThrCysArgAlaSerGlnGlyIleAsnSerTyrLeuAlaTrpTyrGlnGlnLys 60

QY 184 CCAGAGAAGCCCTCAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGAGTGGGTCCA 243
Db 61 ProGlyLysAlaProLysLeuLeuIleTyrValAlaSerThrLeuGlnSerGlyValPro 80

QY 244 TCAAGTTTCAGCGCAGTGGATCTGGACAGATTTTCACTCTCACCATCAGACGCTGCAG 303
Db 81 SerArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGln 100

QY 304 CTGAGAGATTTTGCACCTATTATCTGCGCAACAGTAGTAGTATACCGTACACTTTTGGC 363
Db 101 ProGluAspPheAlaSerTyrTyrCysGlnGlnPheAsnSerTyrProPheThrPheGly 120

QY 364 CAGGGACCAAGCTGAGATCAACGAACTGTGGCT 399
Db 121 GlyGlyThrLysValGluIleArgThrValAla 132

```

RESULT 5

S40333

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40333

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-108/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4,13e-44	Length:	125
Score:	575.00	Matches:	109
Percent Similarity:	94.35%	Conservative:	8
Best Local Similarity:	87.90%	Mismatches:	7
Query Match:	72.69%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-208 (1-439) x S40333 (1-125)

```

QY 16 CCCGTTAGCTCCTCGGGCTCTGCTGCTCTGTTTCCAGGTGCCAGATGTCACATCCAG 75
Db 2 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaLysCysAspIleGln 21

QY 76 ATGACCCAGTCTCCATCTCCTGCTGCTGCTAGGAGACAGAGTACCATCACTTCT 135
Db 22 MetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThrIleThrCys 41

QY 136 CGGCGAGTCAAGGTATTAGCAGCTGGTTAGCTGCTATCAGCAGAAACAGAGAAAGCC 195
Db 42 ArgAlaSerGlnSerIleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAla 61

QY 196 CCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGTTTGCAGTGGGTCCCATCAAGTTTCAGC 255
Db 62 ProLysLeuLeuIleTyrLysAlaSerSerLeuGluSerGlyValProSerArgPheSer 81

QY 256 GSCAGTGTGATCGGACAGATTCTACTCTCACCATCAGCAGCTCAGCCTCAAGATTTT 315
Db 82 GlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspPhe 101

QY 316 GCAACTTATTACTGCCAACAGTATGATAGTTTACCCGTACACTTTTGGCCAGGGGACCAAG 375
Db 102 AlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProTyrThrPheGlyGlnGlyThrLys 121

QY 376 CTGGAGATCAAA 387
Db 122 ValGluIleLys 125

RESULT 6
KHU11
Ig kappa chain precursor V-I region (HK101) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 24-Sep-1999
C:Accession: A01881; A21056
R:Bentley, D.L.; Rabbitts, T.H.
Nucle 288, 730-733, 1980
A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa gene.
A:Reference number: A93241; MUID:81098966; PMID:6779204
A:Accession: A01881
A:Molecule type: DNA
A:Residues: 1-117 <BEN1>
A:Cross-references: GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CAA23824.1; PID:g33176
R:Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: A21056
A:Molecule type: DNA
A:Residues: 1-117 <BEN2>
A:Cross-references: GB:K01322; NID:g185993; PIDN:AAA58930.1; PID:g185994
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:J36264
A:Map position: 2p12-2p12
A:Introns: 19/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1-
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>
F:38-112/Domain: immunoglobulin homology <IMM>
F:45-110/Disulfide bonds: #status predicted
Alignment Scores:
Pred. No.: 6,32e-44 Length: 117
Score: 573.00 Matches: 110
Percent Similarity: 95.73% Conservative: 2
Best Local Similarity: 94.02% Mismatches: 5
Query Match: 72.44% Indels: 0
DB: 1 Gaps: 0

```





C:Accession: S38646  
 R:Bensimon, C.; Chastagner, P.; Zouali, M.  
 submitted to the EMBL Data Library, November 1993  
 A:Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.  
 A:Reference number: S38643  
 A:Accession: S38646  
 A>Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-132 <BEN>  
 A:Cross-references: EMBL:227173; NID:g415961; PIDN:CAA81697.1; PID:g415962  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:40-114/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 9.32e-43 Length: 132  
 Score: 560.00 Matches: 110  
 Percent Similarity: 89.23% Conservative: 6  
 Best Local Similarity: 84.62% Mismatches: 14  
 Query Match: 70.80% Indels: 0  
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S38646 (1-132)

```

QY 1 ATGGACATGAGTTCCTCCCTTCAGCTCTGGGGCTCTGCTCTGTTTCCAGGTGCC 60
DB 3 MetAspMetArgValProAlaGlnLeuLeuLeuGlyLeuLeuLeuTrpLeuProGlyAla 22
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTCACTCTGTCATCTGTAGGAGACAGA 120
DB 23 ArgCysAlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArg 42
QY 121 GTCACCATCACTGTGGCGAGTCAGGGTATTAGCAGTGGTGGTTCAGCTGTTATCAGCAG 180
DB 43 ValThrIleThrCysArgAlaSerGlnGlyIleSerSerTyLeuAlaTrpTyrGlnGln 62
QY 181 AAACAGAGAAAGCCCTAAGTCCCTGATCTTCTGCAATCCAGTTCGAAAGTGGGTC 240
DB 63 LysProGlyLeuAlaProLysLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyVal 82
QY 241 CCATCAAGTTCAGCGGAGTCGATCTGGGACAGATTTCCACTCTCACCATCAGCAGCTG 300
DB 83 ProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeu 102
QY 301 CAGCCTGAAGATTTGCAACTATTACTCCCAACAGTATGATAGTATACCCGTACACTTTT 360
DB 103 GlnSerGluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerTyrProArgThrPhe 122
QY 361 GCCCAGGGACCAAGCTGGAGATCAACGA 390
DB 123 GlyGlnGlyThrLysValGluIleLysArg 132

```

RESULT 10

S40349  
 Ig kappa chain V-J region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
 C:Accession: S40349  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891; PMID:8258341  
 A:Accession: S40349  
 A>Status: preliminary; translation not shown  
 A:Molecule type: mRNA

A:Residues: 1-125 <KLE>  
 A:Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1.75e-42 Length: 125

Score: 557.00 Matches: 109  
 Percent Similarity: 92.00% Conservative: 6  
 Best Local Similarity: 87.20% Mismatches: 10  
 Query Match: 70.42% Indels: 0  
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40349 (1-125)

```

QY 16 CCCGTTACGTCCTGGGGCTCTGCTCTGTTTCCAGGTGCCAGATGTGACATCCAG 75
DB 1 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAlaArgCysAlaIleGln 20
QY 76 ATGACCCAGTCTCCATCTCACTCTGTCATCTGTAGGAGACAGAGTACCACATCACTGT 135
DB 21 LeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40
QY 136 CGGCGAGTCAGGGTATTAGCAGCTGGTTCAGCTGGTATCAGCAAAACACAGAAAGCC 195
DB 41 ArgAlaSerGlnGlyIleSerSerAlaLeuAlaTrpTyrGlnGlnLysProGlyLysAla 60
QY 196 CTTAAGTCCCTGATCTATTCTGCAATCCAGTTCGAAAGTGGGGTCCCATCAAGGTTTCAG 255
DB 61 ProlLysLeuLeuIleTyrAspAlaSerSerLeuGluSerGlyValProSerArgPheSer 80
QY 256 GGCAGTGCATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCTGAAGATTTT 315
DB 81 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
QY 316 GCAACTTATTACTGCAACAGTATGATAGTTACCGGTACACTTTTGGCCAGGGGACCAAG 375
DB 101 AlaThrTyrTyrCysGlnGlnPheAsnThrTyrProLeuThrPheGlyGlyThrLys 120
QY 376 CTGGAGATCAACGA 390
DB 121 ValGluIleLysArg 125

```

RESULT 11

C21056  
 Ig kappa chain precursor V region (HK137) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 21-Jan-2000  
 C:Accession: C21056  
 R:Bentley, D.L.; Rabbitts, T.H.  
 Cell 32, 181-189, 1983  
 A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated  
 A:Reference number: A21056; MUID:83129397; PMID:6402305  
 A:Accession: C21056  
 A>Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-117 <BEN>  
 A:Cross-references: GB:J00248; NID:g185991; PIDN:AAA59094.1; PID:g185992  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:38-112/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 2.68e-42 Length: 117  
 Score: 555.00 Matches: 107  
 Percent Similarity: 95.72% Conservative: 5  
 Best Local Similarity: 91.45% Mismatches: 5  
 Query Match: 70.16% Indels: 0  
 DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x C21056 (1-117)

```

QY 1 ATGGACATGAGTTCCTCCCTTCAGCTCTGGGGCTCTGCTCTGTTTCCAGGTGCC 60
DB 1 MetAspMetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuCysPheProGlyAla 20
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTCCTCAGTCTGTAGGAGACAGA 120
DB 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40

```



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C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7.52e-42 Length: 127  
Score: 550.00 Matches: 109  
Percent Similarity: 91.34% Conservative: 7  
Best Local Similarity: 85.83% Mismatches: 11  
Query Match: 69.53% Indels: 0  
DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40367 (1-127)

```

QY 16 CCGTTTCAGCTCTGGGCTCTGCTCTGTTCCAGGTGCCAGATGTGACATCCAG 75
Db 1 ProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAlaArgCysAspIleGln 20
QY 76 ATGACCCAGTCTCCATCTCTGCTCTGCTCTGCTAGGAGACAGATCCATCCTTGT 135
Db 21 MetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40
QY 136 CGGCGAGTCAAGGTATTAGCAGCTGTAGCCTGTAGCTGTATCAGCAAAACAGAGAACGCC 195
Db 41 ArgAlaSerGlnSerIleSerAsnTrpLeuAsnTrpGlnArgLysProGlyLysAla 60
QY 196 CTAAGTCCCTCATCTATTCTGCTATCCAGTTTGCAGTGGGTCCCATCAAGTTTCAGC 255
Db 61 ProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSer 80
QY 256 GCGAGTGCATCTGGAGCAGATTCTCTCACCATCAGCAGCTTGCCAGCTGAGATTTT 315
Db 81 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
QY 316 GCAACTTATTACTGCCAACAGTAGTAGTTACCCGTACACTTTTGGCCAGGGGACCAAG 375
Db 101 AlaThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGlnGlyThrLys 120
QY 376 CTGAGATCAACGAACTGTG 396
Db 121 ValGluIleLysArgThrVal 127

```

## RESULT 15

S40353  
Ig kappa chain V-J-C region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40353  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40353  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-125 <KLE>  
A;Cross-references: EMBL:X72463  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;30-104/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.14e-41 Length: 125  
Score: 548.00 Matches: 107  
Percent Similarity: 91.20% Conservative: 7  
Best Local Similarity: 85.60% Mismatches: 11  
Query Match: 69.28% Indels: 0  
DB: 2 Gaps: 0

US-08-728-463B-208 (1-439) x S40353 (1-125)

```

QY 25 CTCCTGGGCTCTGCTCTGTTCCAGGTGCCAGATGTGACATCCAGATGACCCAG 84
Db 1 LeuLeuGlyLeuLeuLeuTrpPheProGlyAlaArgCysAspIleGlnMetThrGln 20

```

```

QY 85 TCTCCATCTCTCACTGTCTGCTATCTGTAGGAGACAGAGTCACCATCACTTGTGGGCGAGT 144
Db 21 SerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArgAlaSer 40
QY 145 CAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACAGAGAAAGCCCCCTAAGTCC 204
Db 41 GlnGlyIleGlyAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLysArg 60
QY 205 CTGATCTATTCTGCATCCAGTTTGCAGTGGGTCCCATCAAGGTTTCAGCGGCGAGTGA 264
Db 61 LeuIleTyrAlaAlaSerSerPheGlnSerGlyValProSerArgPheSerGlySerGly 80
QY 265 TCTGGGACAGATTCTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACATTAT 324
Db 81 SerGlyThrGluPheThrLeuThrIleSerGlyLeuGlnProGluAspPheAlaThrTyr 100
QY 325 TACTGCCAACAGTAGTAGTTACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATC 384
Db 101 TyrCysLeuGlnHisAsnSerTyrProLeuThrPheGlyGlyThrArgValGluIle 120
QY 385 AAACGAACTGTGGCT 399
Db 121 LysArgThrValAla 125

```

Search completed: June 3, 2003, 09:07:57  
Job time : 20.5692 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 8.32701 Seconds  
(without alignments)  
4373.264 Million cell updates/sec

Title: US-08-728-463B-208  
Perfect score: 791  
Sequence: 1 ATGCACATGGAGTCCCGT .....CCCGCCATCTCATGAGCTT 439

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame\_n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO spo01/US08728463/runat 03062003 085614 16804/app query.fasta\_1.3690  
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1.1 76 @runat 03062003 085614 16804 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	72.4	117	1 KVI1 HUMAN	P01601 homo sapien
2	529	66.9	129	1 KVI1 HUMAN	P04431 homo sapien
3	528	66.8	117	1 KVI1 HUMAN	P01602 homo sapien
4	489	61.8	108	1 KVI1 HUMAN	P01604 homo sapien
5	487	61.6	108	1 KVI1 HUMAN	P04430 homo sapien
6	486	61.4	129	1 KVI1 HUMAN	P04432 homo sapien
7	476	60.2	108	1 KVI1 HUMAN	P01610 homo sapien
8	470.5	59.5	107	1 KVI1 HUMAN	P01596 homo sapien
9	468	59.2	108	1 KVI1 HUMAN	P01599 homo sapien
10	465	58.8	108	1 KVI1 HUMAN	P01600 homo sapien
11	465	58.8	128	1 KVI1 HUMAN	P01637 mus musculu
12	463	58.5	108	1 KVI1 HUMAN	P01598 homo sapien
13	460	58.2	108	1 KVI1 HUMAN	P01594 homo sapien
14	460	58.2	108	1 KVI1 HUMAN	P01611 homo sapien
15	460	58.2	108	1 KVI1 HUMAN	P01593 homo sapien
16	457	57.8	108	1 KVI1 HUMAN	P01639 mus musculu
17	454	57.4	130	1 KVI1 HUMAN	P01605 mus musculu
18	449	56.8	108	1 KVI1 HUMAN	P01606 homo sapien

19	448	56.6	108	1 KVI1 HUMAN	P01608 homo sapien
20	448	56.6	108	1 KVI1 HUMAN	P03362 homo sapien
21	445	56.3	108	1 KVI1 HUMAN	P01595 homo sapien
22	442.5	55.9	129	1 KVI1 HUMAN	P18136 homo sapien
23	441.5	55.8	129	1 KVI1 HUMAN	P18135 homo sapien
24	441	55.8	108	1 KVI1 HUMAN	P01597 homo sapien
25	441	55.8	108	1 KVI1 HUMAN	P01606 homo sapien
26	438	55.4	108	1 KVI1 HUMAN	P01603 homo sapien
27	433	54.7	108	1 KVI1 HUMAN	P01609 homo sapien
28	428.5	54.2	129	1 KVI1 HUMAN	P04207 homo sapien
29	426	53.9	128	1 KVI1 HUMAN	P06311 homo sapien
30	417	52.7	115	1 KVI1 HUMAN	P06318 mus musculu
31	413	52.2	112	1 KVI1 HUMAN	P01613 homo sapien
32	409	51.7	108	1 KVI1 HUMAN	P01643 mus musculu
33	409	51.7	134	1 KVI1 HUMAN	P06314 homo sapien
34	408.5	51.6	109	1 KVI1 HUMAN	P01612 homo sapien
35	402	50.8	136	1 KVI1 HUMAN	P01634 mus musculu
36	399	50.4	108	1 KVI1 HUMAN	P01636 mus musculu
37	399	50.4	108	1 KVI1 HUMAN	P01644 mus musculu
38	399	50.4	108	1 KVI1 HUMAN	P01652 mus musculu
39	398.5	50.4	109	1 KVI1 HUMAN	P01622 homo sapien
40	398	50.3	114	1 KVI1 HUMAN	P01625 homo sapien
41	397.5	50.3	133	1 KVI1 HUMAN	P06313 homo sapien
42	397.5	50.3	133	1 KVI1 HUMAN	P01620 homo sapien
43	396	50.1	108	1 KVI1 HUMAN	P01650 mus musculu
44	396	50.1	115	1 KVI1 HUMAN	P04433 homo sapien
45	395.5	50.0	109	1 KVI1 HUMAN	P01624 homo sapien

#### ALIGNMENTS

#### RESULT 1

KVI1 HUMAN  
ID KVI1 HUMAN STANDARD; PRT; 117 AA.  
AC P01601;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region HK101 precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81098966; PubMed=6779204;  
RA Bentley D.L., Rabbitts T.H.;  
RT "Human immunoglobulin variable region genes -- DNA sequences of two V  
kappa genes and a pseudogene.";  
RL Nature 288:730-733(1980).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83129397; PubMed=6402305;  
RA Bentley D.L., Rabbitts T.H.;  
RT "Evolution of immunoglobulin V genes: evidence indicating that  
recently duplicated human V kappa sequences have diverged by gene  
conversion.";  
RL Cell 32:181-189(1983).  
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CC EMBL; K01322; AAA58930.1; -  
DR EMBL; K01324; AAA58932.1; -  
DR EMBL; V00558; CAA23824.1; -  
DR PIR; A01881; K1HUI1.  
DR PIR; A21056; A21056.  
DR HSSP; P01607; IREI.

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DR EMBL; X00365; CAA25477.1; ALT\_TERM.  
DR PIR; A01883; KIHOWK.  
DR HSPG; P01607; IREI.  
DR InterPro; IPRO03006; Ig MHC.  
DR InterPro; IPRO03596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGv\_1.  
DR KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129  
FT DOMAIN 23 45 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Alignment Scores:  
Pred. No.: 3,14e-48 Length: 129  
Score: 529.00 Matches: 108  
Percent Similarity: 86.82% Conservative: 4  
Best Local Similarity: 83.72% Mismatches: 17  
Query Match: 66.88% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV1W\_HUMAN (1-129)

QY	1	ATGCACATGGAGTTCCTCCCGTTCCAGCTCCTGGGGCTCTGTGCTGTCTGTTTCCCAGTGCC	60
Dd	1	MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAla	20
QY	61	AGATGTGACATCCAGATCACGCCAGTCTCCATCTCATCTGTGTGATCTGTAGGACAGA	120
Dd	21	ArgCysAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArg	40
QY	121	GTCACCATCACTGTTCGGCGCAGTCAGGGTATTAGCAGCTGTTAGCTGTGATCAGCAG	180
Dd	41	ValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrrLeuAsnTrpTyrrGlnGln	60
QY	181	AAACACAGAGAAGCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTTGCAAAGTGGGCTC	240
Dd	61	LysProGlyLysAlaProLysLeuLeuIleTyrrAlaAlaSerSerLeuGlnSerGlyVal	80
QY	241	CCATCAAGGTTTCAGCGCAGTGGATCTGGNACAGATTTCCTACTCACCATCAGCAGCTG	300
Dd	81	ThrSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu	100
QY	301	CAGCTGAAGATTTTGCACCTTATTACTGCCCCAGATGATGATAGTTACCCGTACACTTTT	360
Dd	101	GlnProGluAspSerAlaThrTyrrTyrrCysGlnGlnSerTyrrSerThrLeuIleThrPhe	120
QY	361	GGCCAGGGGACCAAGCTGGAGATCAA	387
Dd	121	GlyGlnGlyThrArgLeuGluIleLys	129

RESULT 3  
KV1J\_HUMAN  
ID ID\_KV1J\_HUMAN STANDARD; PRT; 117 AA.  
AC AC\_P01602;  
DT DT 21-JUL-1986 (Rel. 01, Created)  
DT DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT DT 15-JUN-1999 (Rel. 38, Last annotation update)  
IG Ig kappa chain V-I region HK102 precursor (Fragment).



```

Db 101 GlyThrLysLeuAspIleLysArg 108
|||||
RESULT 5
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P0430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR HSP; P80362; IWL.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 93 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Alignment Scores:
Pred. No.: 8.77e-44 Length: 108
Score: 487.00
Percent Similarity: 94.44% Matches: 91
Best Local Similarity: 84.26% Conservative: 11
Query Match: 61.57% Mismatches: 6
DB: 1 Indels: 0
Gaps: 0

US-08-728-463B-208 (1-439) x KV1V_HUMAN (1-108)
QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGCTGCTAGGACAGAGTCACC 126
Db 1 AspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTCGGCGAGTCAGGTATTACAGCTGTTAGCTGTTATCAGCAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerValThrAsnThrValAlaTrpPheGlnGlnLysPro 40
QY 187 GAGAAAGCCCTAAGTCCCTGATCTATCTGTCATGCTGCAAGTTCGAAAGTGGGTCCTCA 246
Db 41 GlyLysAlaProLysSerLeuLeuThrAspAlaSerThrLeuGlnSerGlyValProSer 60
QY 247 AGTTTCAGCGCGAGTGGATCTGGGACAGATTTCACTCTCACCACAGCCTGCGAGCT 306
Db 61 AsnPheThrGlySerGlyThrAspPheLeuLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACCTATTACTGCCAAGATGATAGTACCTACCGTACACTTTTGGCCAG 366
Db 81 GluAspPheAlaThrTyThrCysGlnGlnLysThrAsnSerTyProTyThrPheGlyGln 100
QY 367 GGGACCAAGCTGGAGATCAACCA 390
Db 101 GlyThrLysValGlnIleLysArg 108

```

```

RESULT 6
KV1X_HUMAN
ID KV1X_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC or send an email to license@sib-sib.ch).
CC -----
EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; KIHU1.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

Alignment Scores:
Pred. No.: 1.15e-43 Length: 129
Score: 486.00 Matches: 95
Percent Similarity: 82.95% Conservative: 12
Best Local Similarity: 73.64% Mismatches: 22
Query Match: 61.44% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV1X_HUMAN (1-129)
QY 1 ATGCAGATGGAGTCCCGCTTCAGCTCTGGGGCTCTGCTGCTGTTCACAGTGCC 60
Db 1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuArgVal 20
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCTCCTGCTGCTAGGACAGAG 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40
QY 121 GTCACCATCCTGTCGGCGAGTCAGGTATTACAGCTGTTAGCTGTTATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaGlyHisAsnIleThrAsnPheLeuSerTrpTyThrGln 60
QY 181 AAACGAGAGAAAGCCCTAAGTCCCTGATCTATCTGTCATGCTGCTGCAAGTGGGTC 240

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Db 61 LysProGlyLysAlaProThrLeuLeuLeuLeuLeuLeuValGlyVal 80  
QY 241 CCATCAGAGTTGAGCGGAGTGGATCTGGACAGATTTCACCTCTCACCATCAGAGCCG 300  
Db 81 ProSerArgPheSerGlySerGlyAlaGluPheThrLeuThrLeuThrLeu 100  
QY 301 CAGCGTGAAGATTTGCACTTATTACTCCCAACAGTATGATAGTTACCGGTACACTTTT 360  
Db 101 GlnProGluAspPheAlaThrTyrcysGlnGlnAsnTyrcysPheSerPheThrPhe 120  
QY 361 GCGCAGGGGACCAAGCTGGAGATCAA 387  
Db 121 GlyGlyGlyThrLysValAspAsnLys 129

## RESULT 7

KVID\_HUMAN  
ID KVID\_HUMAN STANDARD; PRT; 108 AA.  
AC P01610;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Ig kappa chain V-I region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
(protein WEA) with antibody activity against 3,4-pyruvylated  
galactose in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
WALDENSTROM'S MACROGLOBULINEMIA.  
DR PIR; A01876; KIHUE.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region; Monoclonal antibody.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

## Alignment Scores:

Pred. No.: 1.29e-42 Length: 108  
Score: 476.00 Matches: 91  
Percent Similarity: 91.67% Conservative: 8  
Best Local Similarity: 84.26% Mismatches: 9  
Query Match: 60.18% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KVID\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGCTGCTGCTAGGACAGAGTCACC 126  
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
QY 127 ATCACTTGTGGCGGAGTCAGGATATTAGCAGCTGGTGGTATCAGCAGAAACCA 186  
Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpThrGlnLysPro 40

QY 187 GGAAGAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAAGTGGGTCCCATCA 246  
Db 41 GlyThrAlaProLysArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGCTGCAGCT 306  
Db 61 ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80  
QY 307 GAAGATTGCAACTTATTACTGCGCAACAGATGATAGTACCCGTCACATTTTGGCCAG 366  
Db 81 GluAspPheAlaThrTyrcysLeuGlnTyrcysSerPheProTrpThrPheGlyGln 100  
QY 367 GCGACCAAGCTGGAGATCAAACA 390  
Db 101 GlyThrLysValGluValLysArg 108

## RESULT 8

KVID\_HUMAN  
ID KVID\_HUMAN STANDARD; PRT; 107 AA.  
AC P01596;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Ig kappa chain V-I region CAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75075135; PubMed=4216454;  
RA Milstein C.P., Deverson E.V.;  
RT "Primary structure of kappa light chain from a human myeloma  
protein.";  
RL Eur. J. Biochem. 49:377-391 (1974).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01864; KIHUAR.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region; Glycoprotein.  
FT CARBOHYD 28 28  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

## Alignment Scores:

Pred. No.: 4.94e-42 Length: 107  
Score: 470.50 Matches: 89  
Percent Similarity: 93.52% Conservative: 12  
Best Local Similarity: 82.41% Mismatches: 6  
Query Match: 59.48% Indels: 1  
DB: 1 Gaps: 1

US-08-728-463B-208 (1-439) x KVID\_HUMAN (1-107)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGCTGCTGCTAGGACAGAGTCACC 126  
Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValAla 20  
QY 127 ATCACTTGTGGCGGAGTCAGGATATTAGCAGCTGGTGGTATCAGCAGAAACCA 186  
Db 21 IleThrCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpThrGlnLysPro 40  
QY 187 GGAAGAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAAGTGGGTCCCATCA 246  
Db 41 GlyLysAlaProLysValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
QY 247 AGGTTTCAGCGGAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGCTGCAGCT 306

Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu\*\*\*Pro 80  
 QY 307 GAAGATTTCGCACTTATTACTCCCAACAGTATGATAGTACCGTACACTTTTGGCCAG 366  
 Db 81 \*\*\*\*\*PheAlaThrTyTyCysGlnGlnTyAsnThrPhe---PheThrPheGlyPro 99  
 QY 367 GGGACCAAGCTGGAGATCAAAACA 390  
 Db 100 GlyThrLysValAspIleLysarg 107

RESULT 9  
 KVIG\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01599;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region GHL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 RT kappa-type, subgroup I."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN  
 DR PIR; A01867; KIHUCL.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV\_1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; C1AD3CB0F600FF73 CRC64;

Alignment Scores:  
 Pred. No.: 9,11e-42 Length: 108  
 Score: 468.00 Matches: 91  
 Percent Similarity: 91.67% Conservative: 8  
 Best Local Similarity: 84.26% Mismatches: 9  
 Query Match: 59.17% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463b-208 (1-439) x KVIG\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGACAGAGTACC 126  
 Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGGCGAGTCAGGGTATTACACCTGGTGGTATCAGCAGAAACA 186  
 Db 21 IleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpTyGlnGlnysPro 40  
 QY 187 GAGAAAGCCCTTAAGTCCCTGATCTTCTGTCATCCAGTTTGCAGAGTGGGGTCCCATCA 246  
 Db 41 GlyLysAlaProGlyGluLeuIleTyAlaAlaSerAsnLeuGlnSerGlyValProSer 60

QY 247 AGTTTCAGCGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTTCAGCCT 306  
 Db 61 ArgPheSerGlySerGlyAlaGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80  
 QY 307 GAAGATTTCGCACTTATTACTCCCAACAGTATGATAGTACCGTACACTTTTGGCCAG 366  
 Db 81 GLUAspPheAlaThrTyTyCysLeuGlnGlnAsnSerTyProArgSerPheGlyGln 100  
 QY 367 GGGACCAAGCTGGAGATCAAAACA 390  
 Db 101 GlyThrLysValGluIleLysarg 108

RESULT 10  
 KVIG\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Hau.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 RT subgroups."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01868; KIHUHU.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV\_1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 08D3A6160D8D0618 CRC64;

Alignment Scores:  
 Pred. No.: 1,9e-41 Length: 108  
 Score: 465.00 Matches: 92  
 Percent Similarity: 91.67% Conservative: 7  
 Best Local Similarity: 85.19% Mismatches: 9  
 Query Match: 58.79% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463b-208 (1-439) x KVIG\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGACAGAGTACC 126  
 Db 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 127 ATCACTTGTGGCGAGTCAGGGTATTACACCTGGTGGTATCAGCAGAAACA 186  
 Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyLeuSerTrpTyGlnGlnysPro 40  
 QY 187 GAGAAAGCCCTTAAGTCCCTGATCTTCTGTCATCCAGTTTGCAGAGTGGGGTCCCATCA 246  
 Db 41 GlyLysAlaProGlnValLeuIleTyAlaAlaSerSerLeuProSerGlyValProSer 60

QY 247 AGGTTACGGCAGTGGATCTGGACAGATTTCACCTCTCACCATCAGCAGCCTGCAGCCT 306  
 |||||  
 Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
 |||||  
 QY 307 GAAGATTGTCACCTATTACTGCGCAACAGTAGTATGATGTTACCCGTCACACATTTTGGCCAG 366  
 |||||  
 Db 81 GluAppPheAlaThrTyTyCysGlnGlnAsnTyIleThrProThrSerPheGlyGln 100  
 |||||  
 QY 367 GGGACCAAGCTGGAGATCAACGA 390  
 |||||  
 Db 101 GlyThrArgValGluIleLysArg 108  
 |||||

RESULT 11  
KVSE\_MOUSE

ID KVSE\_MOUSE STANDARD; PRT; 128 AA.  
 AC P01637;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region T1 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=81052342; PubMed=6776411;  
 RX Altenburger W., Steinmetz M., Zachau H.G.;  
 RT "Functional and non-functional joining in immunoglobulin light chain  
 genes of a mouse myeloma.";  
 RL Nature 287:603-607(1980).  
 CC -----  
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 CC -----

DR EMBL; V00772; CAA24150.1; -.  
 DR PIR; A01920; KVMST1.  
 DR HSP; P80382; LWTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 69 FRAMEWORK-2.  
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 77 108 FRAMEWORK-3.  
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 118 127 FRAMEWORK-4.  
 FT DISULFID 43 108 BY SIMILARITY.  
 FT NON\_TER 128 128  
 SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

## Alignment Scores:

Pred. No.: 1,94e-41 Length: 128  
 Score: 465.00 Matches: 85  
 Percent Similarity: 82.03% Conservative: 19  
 Best Local Similarity: 67.19% Mismatches: 23  
 Query Match: 58.79% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KVSE\_MOUSE (1-128)

QY 7 ATGGAGTCCCGTTCAGCTCTCTGGGCTCTGTGCTGTCTGTTCACGAGTCCAGATGT 66

Db 1 MetArgThrProAlaGlnPheLeuGlyIleLeuLeuLeuTrpPheProGlyIleLysCys 20  
 |||||  
 QY 67 GACATCCAGATGACCCAGTCTCCATCTCTCATCTGTGTCATCTGTAGGACAGAGTCACC 126  
 |||||  
 Db 21 AspileLysMetThrGlnSerProSerMetTyrAlaSerLeuGlyGluArgValThr 40  
 |||||  
 QY 127 ATCACTTCTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGTATCATCAGCAGAACCA 186  
 |||||  
 Db 41 IleSerCysLysAlaSerGlnAspIleAsnSerTyrLeuThrTrpPheGlnGlnLysPro 60  
 |||||  
 QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAAAAGTGGGTCCCATCA 246  
 |||||  
 Db 61 GlyLysSerProLysThrLeuLeuTyrArgAlaAsnArgLeuValAspGlyValProSer 80  
 |||||  
 QY 247 AGGTTACGGCAGTGGATCTGGACAGATTTCACCTCTCACCATCAGCAGCCTGCAGCCT 306  
 |||||  
 Db 81 ArgPheSerGlySerGlyThrGlnAspPheSerLeuThrIleSerSerLeuGluTyr 100  
 |||||  
 QY 307 GAAGATTGTCACCTATTACTGCGCAACAGTAGTATGATGTTACCCGTCACACATTTTGGCCAG 366  
 |||||  
 Db 101 GluAppMetGlyIleTyrTyCysLeuGlnTyrAspGluPheProLeuThrPheGlyAla 120  
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 QY 367 GGGACCAAGCTGGAGATCAACGA 390  
 |||||  
 Db 121 GlyThrLysLeuGluLysArg 128  
 |||||

RESULT 12  
 KVIF\_HUMAN  
 ID KVIF\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01598;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=71064023; PubMed=5489770;  
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
 RT acid sequence of the light chain.";  
 RL Biochemistry 9:3155-3161(1970).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01866; KIHUEU.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

## Alignment Scores:

Pred. No.: 3,09e-41 Length: 108  
 Score: 463.00 Matches: 88  
 Percent Similarity: 91.59% Conservative: 10  
 Best Local Similarity: 82.24% Mismatches: 9  
 Query Match: 58.53% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV1F\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGTCATCTGTCATCTGTAGGAGACAGAGTACC 126  
 |||||  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20

QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGTGTATCAGCAGAAACCA 186  
 |||||  
 Db 21 IleThrCysArgAlaSerGlnSerIleAenThrTrpLeuAlaTrpTyGlnGlnLysPro 40

QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGGAGTGGGTCATCA 246  
 |||||  
 Db 41 GlyLysAlaProLysLeuLeuMetTyLysAlaSerSerLeuGluSerGlyValProSer 60

QY 247 AGTTTCAGCGGAGTGGAGTCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCT 306  
 |||||  
 Db 61 ArgPheIleGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80

QY 307 GAAGATTGTGCACTTATTACTGCAACAGTATGATGTTACCCGTACACTTTTGGCCAG 366  
 |||||  
 Db 81 AspPheAlaThrTyTyCysGlnGlnTyAsnSerAspSerLysMetPheGlyGln 100

QY 367 GGGACCAAGCTGGAGATCAAA 387  
 |||||  
 Db 101 GlyThrLysValGluValLys 107

## RESULT 13

KV1B\_HUMAN  
 ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein Au).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Fehlinhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RT Bence-Jones protein Au.";  
 RL Biophys. Struct. Mech. 1:139-146 (1975).  
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REI.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01862; K1HUAU.  
 DR HSSP; P01607; 1REI.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.

Immunoglobulin V region; Bence-Jones protein.  
 KW DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 FRAMEWORK-4.  
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 23 88 FRAMEWORK-4.  
 FT NON TER 108 BY SIMILARITY.

SQ SEQUENCE 108 AA; 11939 MW; E8011187E56F6FB9 CRC64;

## Alignment Scores:

Pred. No.: 6.43e-41 Length: 108  
 Score: 460.00 Matches: 89  
 Percent Similarity: 87.96% Conservative: 6  
 Best Local Similarity: 82.41% Mismatches: 13  
 Query Match: 58.15% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV1B\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGTCATCTGTAGGAGACAGAGTACC 126  
 |||||  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerValGlyAspArgValThr 20

QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGTGTATCAGCAGAAACCA 186  
 |||||  
 Db 21 IleThrCysGlnAlaSerGlnAspIleSerAspTyLysAenThrTyGlnGlnLysPro 40

QY 187 GAGAAAGCCCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAGGAGTGGGTCATCA 246  
 |||||  
 Db 41 GlyLysAlaProLysLeuLeuIleTyAspAlaSerAsnLeuGluSerGlyValProSer 60

QY 247 AGTTTCAGCGGAGTGGAGTCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCT 306  
 |||||  
 Db 61 ArgPheSerGlyGlyGlySerGlyAlaPheThrPheThrIleSerSerLeuGlnPro 80

QY 307 GAAGATTGTGCACTTATTACTGCAACAGTATGATGTTACCCGTACACTTTTGGCCAG 366  
 |||||  
 Db 81 GluAspIleAlaThrTyTyCysGlnGlnTyAspTyLysProTrpThrPheGlyGln 100

QY 367 GGGACCAAGCTGGAGATCAAAACGA 390  
 |||||  
 Db 101 GlyThrLysValGluIleLysArg 108

## RESULT 14

KV1O\_HUMAN  
 ID KV1O\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01607;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-I region Rel.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76023758; PubMed=809329;  
 RA Palm W., Hilschmann N.;  
 RT "The primary structure of a crystalline monoclonal immunoglobulin  
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation  
 RT and characterization of the tryptic peptides; the complete amino acid  
 RT sequence of the protein; a contribution to the elucidation of the  
 RT three-dimensional structure of antibodies, in particular their  
 RT combining site.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=76039968; PubMed=1182131;  
 Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;

RT "The molecular structure of a dimer composed of the variable portions  
RL of the Bence-Jones protein REI refined at 2.0-A resolution."  
RT Biochemistry 14:4943-4952(1975).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)  
CC MARKER.

CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01873; KIHURE;  
DR PDB; 1REI; 17-FEB-84.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT STRAND 4 7  
FT STRAND 10 13  
FT STRAND 15 16  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49  
FT TURN 50 52  
FT STRAND 53 54  
FT TURN 56 57  
FT TURN 60 61  
FT STRAND 62 67  
FT TURN 68 69  
FT STRAND 70 75  
FT TURN 80 82  
FT HELIX 85 90  
FT STRAND 98 98  
FT STRAND 102 106  
FT STRAND 108 108  
FT NON TER 108 108  
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Alignment Scores:  
Pred. No.: 6,43e-41 Length: 108  
Score: 460.00 Matches: 89  
Percent Similarity: 87.9% Conservative: 6  
Best Local Similarity: 82.4% Mismatches: 13  
Query Match: 58.1% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KV10\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGCTGCTAGGACAGAGTCACC 126  
DB 1 AspileGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArgValThr 20  
QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGTGTGAGCTGTATCAGCAGAAACCA 186  
DB 21 IleThrCysGlnAlaSerGlnAspilelleLysTyrLeuAsnTyrThrGlnThrPro 40  
QY 187 GAGAAAGCCCTTAAGTCCCTGATCTATCTGCTAGTTTCCAAAGTGGGTCCCATCA 246  
DB 41 GlyLysAlaProLysLeuLeuIleTyrGluAlaSerAsnLeuGlnAlaGlyValProSer 60  
QY 247 AGTTTCAGGCGGAGTGGATCTGGACAGATTTTCACTCTCACCATCAGAGCCCTGAGCCT 306  
DB 61 ArgPheSerGlySerGlySerGlyThrAspTyrThrPheThrIleSerSerLeuGlnPro 80  
QY 307 GAAGATTTTGCACCTATTACTGCCAACAGTATGATGTTACCCGTACACTTTTGGCCAG 366  
DB 81 GluAspileAlaThrTyrTyrCysGlnGlnTyrGlnSerLeuProTyrThrPheGlyGln 100

QY 367 GGGACCAAGCTGGAGATCAAAACGA 390  
DB 101 GlyThrLysLeuGlnIleThrArg 108

RESULT 15

KVIS\_HUMAN  
ID KVIS\_HUMAN STANDARD; PRT; 108 AA.  
AC P01611;

DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-1 region Wes.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RA MEDLINE=81092279; PubMed=6778806;

RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;

RT "Preparative separation of the tryptic hydrolysate of a protein by  
RT high-pressure liquid chromatography. The primary structure of a  
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein  
RT Wes)."

RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01877; KIHUWS.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23

FT DOMAIN 24 34

FT DOMAIN 35 49

FT DOMAIN 50 56

FT DOMAIN 57 88

FT DOMAIN 89 97

FT DOMAIN 98 107

FT DISULFID 23 88

FT NON TER 108 108

SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Alignment Scores:

Pred. No.: 6,43e-41 Length: 108  
Score: 460.00 Matches: 90  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 83.3% Mismatches: 11  
Query Match: 58.1% Indels: 0  
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x KVIS\_HUMAN (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTGCTGCTAGGACAGAGTCACC 126  
DB 1 AspileGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArgValThr 20

QY 127 ATCACTTGTGGCGGAGTCAGGATTTAGCAGTGTGAGCTGTATCAGCAGAAACCA 186  
DB 21 IleThrCysArgAlaSerGlnAspileSerHisTyrLeuAlaTyrThrGlnGlnLysSer 40

QY 187 GAGAAAGCCCTTAAGTCCCTGATCTATCTGCTAGTTTCCAAAGTGGGTCCCATCA 246  
DB 41 GlyLysAlaProLysLeuLeuIleTyrSerAlaSerLeuGlnAsnGlyValProSer 60

QY 247 AGTTTCAGGCGGAGTGGATCTGGACAGATTTTCACTCTCACCATCAGAGCCCTGAGCCT 306  
DB 61 ArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80

QY 307 GAAGATTTTGCACCTATTACTGCCAACAGTATGATGTTACCCGTACACTTTTGGCCAG 366

Tue Jun 3 09:41:06 2003

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Page 10

Db 81 GluaspPheAlaThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100  
Qy 367 GGGACCAAGCTGGAGATCAAACGA 390  
Db 101 GlyThrThrValaspIleLysArg 108

Search completed: June 3, 2003, 09:04:07  
Job time : 10.327 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 38.9704 Seconds  
(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGCACATGGAGTTCCTCCCGT.....CCCGCCATCTGATGAGCTT 439

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2 1/USPTO spool/US08728463/runat 03062003 085614 16815/app query.fasta\_1.3690  
-DB=SPTRMBL 21 -QWMT=fastcan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CGN 1 1 380 @runat 03062003 085614 16815 -NCPV=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	539	68.1	234	11 Q8R062	Q8R062 mus musculus

ID	Q8R062	PRELIMINARY	PRT	234 AA
2	523	66.1	234	11 Q8VCP0
3	510	64.5	233	11 Q8VCP0
4	506	64.0	234	11 Q8VCP0
5	492	62.2	108	4 Q8VCP0
6	473	59.8	108	4 Q8VCP0
7	464	58.7	108	4 Q8VCP0
8	463.5	58.6	107	4 Q8VCP0
9	459	58.0	214	11 Q8VCP0
10	453	57.3	116	4 Q8VCP0
11	445	56.3	127	11 Q8VCP0
12	444.5	56.2	239	4 Q8VCP0
13	438.5	55.4	107	4 Q8VCP0
14	411	52.0	238	11 Q8VCP0
15	405	51.2	108	11 Q8VCP0
16	404	51.1	298	11 Q8VCP0
17	400	50.6	107	11 Q8VCP0
18	399	50.4	109	11 Q8VCP0
19	397	50.2	108	4 Q8VCP0
20	395	49.9	238	11 Q8VCP0
21	391.5	49.5	235	11 Q8VCP0
22	390.5	49.4	239	11 Q8VCP0
23	389.5	49.2	109	4 Q8VCP0
24	385.5	48.7	134	11 Q8VCP0
25	385	48.7	234	11 Q8VCP0
26	383.5	48.5	109	4 Q8VCP0
27	371.5	47.0	109	4 Q8VCP0
28	364	46.0	111	11 Q8VCP0
29	357.5	45.2	241	11 Q8VCP0
30	344.5	43.6	106	5 Q8VCP0
31	341	43.1	107	11 Q8VCP0
32	328	41.5	99	11 Q8VCP0
33	325	41.1	97	11 Q8VCP0
34	321	40.6	101	11 Q8VCP0
35	313	39.6	103	11 Q8VCP0
36	303	38.3	114	4 Q8VCP0
37	299	37.8	109	6 Q8VCP0
38	297.5	37.6	104	11 Q8VCP0
39	295.5	37.4	237	4 Q8VCP0
40	288.5	36.5	237	4 Q8VCP0
41	288.5	36.5	237	4 Q8VCP0
42	258	32.6	236	4 Q8VCP0
43	248	31.4	130	4 Q8VCP0
44	242	30.6	235	11 Q8VCP0
45	237.5	30.0	112	4 Q8VCP0

## ALIGNMENTS

RESULT 1

Q8R062  
ID Q8R062  
AC Q8R062  
DT 01-JUN-2002 (TRENDEL, 21, Created)  
DT 01-JUN-2002 (TRENDEL, 21, Last sequence update)  
DT 01-JUN-2002 (TRENDEL, 21, Last annotation update)  
DE Hypothetical 25.9 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC027418; AAH27418.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426ABAB1 CRC64;

Alignment Scores:

Pred. No.: 1,71e-52 Length: 234  
Score: 539.00 Matches: 103  
Percent Similarity: 84.06% Conservative: 13





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Db      30 LeuSerAlaSerLeuGlyAspArgValThrIleSerCysSerGlySerGlnGlyIleAla 49
      157 AGCTGGTGTAGCTGTATCAGCAGAAACAGAGAGCCCTAAGTCCCTGATCTATTCT 216
      50 AsnTyrLeuAsnTrpTyrGlnGlnLysProAspGlyThrValLysLeuLeuIleTyr 69
      217 GCATCCAGTTTCAAGTGGGTCCCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAT 276
      70 ThrSerSerLeuHisSerGlyValProSerArgPheSerGlySerGlySerGlyThrAsp 89
      277 TTCACTCTCACCATCAGCAGCTGAGCCTGAGGCTGAAGATTTTGGCAACTATTACTGCCAACAG 336
      90 TyrSerLeuThrIleSerAsnLeuGluProGluAspIleAlaThrTyrTyrCysGlnGln 109
      337 TATGATAGTTACCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACAAAGTGTG 396
      110 TyrArgTyrLeuProTrpTrpPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAsp 129
      397 GCTGCACCATCTGTCTTCATCTCTCCGCCCATCTGTGAA 435
      130 AlaAlaProThrValSerIlePheProProSerSerGlu 142

RESULT 4
Q91WF8
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; Iq_MHC.
DR Pfam; PF00047; Iq; 2.
DR SMART; SM00406; Iq; 1.
DR PROSITE; PS00290; Iq_MHC; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B056EB7812D2 CRC64;

Alignment Scores:
Pred. No.: 9.69e-49 Length: 234
Score: 506.00 Matches: 98
Percent Similarity: 82.61% Conservative: 16
Best Local Similarity: 71.01% Mismatches: 24
Query Match: 63.9% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-208 (1-439) x Q91WF8 (1-234)

QY 22 CAGCTCTGGGGCTCTGCTGCTCTGTTTCCAGGTGCGAGATGTGATCCAGATGACC 81
Db 6 GlnPheLeuGlyLeuLeuLeuLeuCysPheGlnGlyThrArgCysAspIleGlnMetThr 25
QY 82 CAGTCTCCATCTCCTACTGTCTGATCTGTAGGAGCAGAGTCCACATCACTGTCTGGGG 141
Db 26 GlnThrThrSerSerLeuSerAlaSerLeuGlyAspArgValThrIleSerCysArgAla 45
QY 142 ACTCAGGGTATTAGCAGCTGGTGTAGCTGTATCAGCAGAAACCAAGAGAACCCCTAAG 201
Db 46 SerGlnAspIleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProAspGlyThrValLys 65
QY 202 TCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGTGCCATCAAGGTTTCAGCGCAGT 261

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Db      66 LeuLeuIleTyrTyrThrSerArgLeuTyrLeuGlyValProSerArgPheSerGlySer 85
      262 GGATCTGGGACAGATTCTCACTCTCACCATCAGCAGCCTGCAGCCTCAAGATTTTGCACCT 321
      86 GlySerGlyThrAspTyrSerLeuThrIleSerAsnLeuGluGlnGluAspIleAlaThr 105
      322 TATTACTGCCACAGTATGATGATTACCGGTACACTTTTGGCCAGGGGACCAAGCTGGAG 381
      106 TyrPheCysGlnGlnGlyAsnThrProProPheThrPheGlySerGlyThrLysLeuGlu 125
      382 ATCAAAACGAACCTGTGCTGCACCATCTGTCTTCATCTTCCCGCCCATCTGTATGAA 435
      126 ValLysArgAlaAspAlaAlaProThrValSerIlePheProProSerSerGlu 143

RESULT 5
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035044; RAD56280.1; -.
DR HSP; F01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
DR NON_TER 1 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Alignment Scores:
Pred. No.: 3.31e-47 Length: 108
Score: 492.00 Matches: 96
Percent Similarity: 94.44% Conservative: 6
Best Local Similarity: 88.89% Mismatches: 6
Query Match: 62.20% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-208 (1-439) x Q9UL70 (1-108)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCACTGTCTGTCATCTGTAGGAGACAGATCACC 126
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGGGCGAGTCAGGGTATTAGCAGCTGGTGTAGCTGTATCAGCAGAAACCA 186
Db 21 IleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40
QY 187 GAGAAGCCCTCAAGTCCCTGATCTATCTTCATCTCAGTTTGCAAAGTGGGTGCCATCA 246
Db 41 GlyLysValProLysSerLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 60
QY 247 AGGTTTCAGGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCT 306
Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY 307 GAAGATTTTGCACACTTATTACTTGCACACAGTATGATAGTTACCCCGTACACTTTTGGCCAG 366

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Db      81 GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
QY      367 GGGACCAAGCTGGAGATCAACGA 390
Db      101 GlyThrLysLeuGluIleLysArg 108
RESULT 6
Q9UL77
ID      Q9UL77 PRELIMINARY; PRT; 108 AA.
AC      Q9UL77;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      Myosin-reactive immunoglobulin light chain variable region
DE      (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR      EMBL; AF035037; AAD56273.1; -.
DR      HSSP; P01607; IREI.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; IG_1.
DR      SMART; SM00406; IGV_1.
FT      NON_TER 1
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Alignment Scores:
Pred. No.: 4,78e-45 Length: 108
Score: 473.00 Matches: 94
Percent Similarity: 91.67% Conservative: 5
Best Local Similarity: 87.04% Mismatches: 9
Query Match: 59.80% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-208 (1-439) x Q9UL77 (1-108)
QY      67 GACATCCAGATGCCAGTCTCCATCTCTGTCATCTGTAGGACAGAGTCACC 126
Db      1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY      127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGTTAGCTGGTATCAGCAAAACCA 186
Db      21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro 40
QY      187 GAGAAAGCCCTTAAGTCCCTGATCTTCTGCATCCAGTTTCCAAAGTGGGTCCCATCA 246
Db      41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60
QY      247 AGGTTACGGCGAGTCGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306
Db      61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80
QY      307 GAAGATTTTGCACCTATTACTGCCAACAGATGATAGTACCCTGACACTTTTGGCCAG 366
Db      81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrSerPheProThrPheGlyGlu 100
QY      367 GGGACCAAGCTGGAGATCAACGA 390
Db      101 GlyThrLysValGluIleLysArg 108
RESULT 7
Q9UL79
ID      Q96SA9 PRELIMINARY; PRT; 107 AA.
AC      Q96SA9;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE      variable region (Fragment).
OS      Homo sapiens (Human).

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QY 172 TATCAGCAGAACACGAGAACCCCTAAGTCCCTGATCTATCTGTCATCCAGATTGGCAA 231
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
QY 232 AGTGGGGTCCCATCAAGGTTACGGCGCAGTGGATCTGGGACAGATTTCTCCTCACCAC 291
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
QY 292 AGCAGCTGACGCTGAGATTTTGCATTTACTTACTGCAACAGATGATGATGATGATGAT 351
Db 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120
QY 352 TACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACAGACTGCTGGCTGCACCATCTGTC 411
Db 121 SerThrPheGlyGlnGlyThrLysLeuGluIleLysArgThrValAlaAlaProSerVal 140
QY 412 TTCACTTCTCCCGCCATCTGATCAA 435
Db 141 PheIlePheProProSerAspGlu 148

RESULT 13
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe F.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; RAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

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## Alignment Scores:

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Pred. No.: 48-41 Length: 107
Score: 438.50 Matches: 90
Percent Similarity: 88.07% Conservative: 6
Best Local Similarity: 82.57% Mismatches: 10
Query Match: 55.44% Indels: 3
DB: 4 Gaps: 2

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US-08-728-463B-208 (1-439) x Q9UL81 (1-107)

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QY 67 GACATCCAGATGACCCAGTCTCCATCTCTGTCATCTGTAGGAGACAGATGACC 126
Db 1 AsplieGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20
QY 127 ATCACTTGTGGCGAGTCAGGGTATTACAGCTGTTAGCTGTGATCAGGAGAACCA 186
Db 21 IleThrCysArgAlaSerGlnSerIleSerAsnTyrLeuAsnTrpTyrGlnGlnLysPro 40
QY 187 GAGAAGGCCCTCAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAGTGGGTCCCATCA 246
Db 41 GlyLysAlaProAsnLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProser 60

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QY 247 AGTTTCAGCGCAGTGGATCTGGGACAGATTTCTACTCTCACCATCAGCAGCTGCAGCCT 306
Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAla 80
QY 307 GAAGATTTTGAACACTTATTACTGCGCAACAGATGATGATGATGATGATGATGATGAT 363
Db 81 GlusaspPheAlaThrTyrTyrCysGlnGln-----SerTyrSerAlaLeuThrPheGly 98
QY 364 CAGGGACCAAGCTGAGATCAAAACGA 390
Db 99 ProGlyThrLysValAspIleArgArg 107

RESULT 14
Q99M37
ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Alignment Scores:
Pred. No.: 6,17e-38 Length: 238
Score: 411.00 Matches: 83
Percent Similarity: 70.27% Conservative: 21
Best Local Similarity: 56.08% Mismatches: 38
Query Match: 51.96% Indels: 6
DB: 11 Gaps: 2

US-08-728-463B-208 (1-439) x Q99M37 (1-238)
QY 7 ATGGAGTTCCTCCGTTACGCTCTGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 66
Db 1 MetLysLeuProValArgLeuLeu---ValLeuMetPheTrpIleProAlaSerSerSer 19
QY 67 GACATCCAGATGACCCAGTCTCCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCT 126
Db 20 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 39
QY 127 ATCACTTGTGGCGAGTCAGGGTATT-----AGCAGCTGGTTAGCTCG 171
Db 40 IleSerCysArgSerSerGlnSerIleValHisSerAsnGlyAsnThrTyrLeuGluTrp 59
QY 172 TATCAGCAGAACACGAGAACCCCTAAGTCCCTGATCTATCTGTCATCCAGATTGGCAA 231
Db 60 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 79
QY 232 AGTGGGTCCCATCAAGTTGAGGTCAGCGCAGTGGATCTGGGACAGATTTCTCCTCACCAC 291

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||||| ||| |||:::|||||:::|||||
Db      81  GluAspLeuAlaGlnTyrPheCysGlnGlnTyrAsnSerTyrProTyrThrPheGlyGly 100

|||||
QY      367  GGGACCAAGCTGGAGATCAACGA 390

|||||
Db      101  GlyThrIysLeuGluIleLysArg 108

Search completed: June 3, 2003, 09:15:55
Job time : 40.9704 secs

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Search completed: June 3, 2003, 09:15:55  
Job time : 40.9704 secs

PRT;

Alignment Scores:	
Read No.:	2:59e-37
Score:	405.00
Percent Similarity:	85.1%
Percent Local Similarity:	70.3%
Every Match:	51.20%
B:	11
Gaps:	0
Length:	108
Matches:	76
Conservative:	16
Mismatches:	16
Indels:	1

Red. No.:	2:59e-37	Length:	108
Core:	405.00	Matches:	76
Percent Similarity:	85.19%	Conservative:	16
Best Local Similarity:	70.37%	Mismatches:	16
Query Match:	51.20%	Indels:	0
B:	11	Gaps:	0

67	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGAGACAGAGTCACC	126
b		
1	AspileValMetThrGlnSerGlnThrPheMetSerThrSerValGlyAspArgValSer	20
127	ATCACTTGTTCGGCGCAGTCAGGCTATTACAGACTGGTTAGCTCGTATCAGCAAAACCA	186
b		
21	ValThrCysIysAlaSerGlnAsnValGlyThrAsnValAlaTrpTyrGlnGlnLysPro	40
187	GAGAAAGCCCTTAAGTCCCTCGATCTATTCTGCATCCAGCTTTTGCAAAAGTGGGTCCCATCA	246
b		
41	GlyGlnSerProLysAlaLeuIleTyrSerAlaSerTyrProTyrSerGlyValProHis	60
247	AGGTTTCAGCGGCAGTCGGATCTGGACAGATTCACTCTCACCATCAGCAGCCTGACGCT	306
b		
61	ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerAsnValGlnSer	80
307	CGAGATTTTGCAACTATTATTCTGCCAACAGTATGATAGTTACCCGTACACTTTTGGCCAG	366

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 28.3951 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGGACATGGAGTTCCTCCGT.....CCGGCCTCTGATGAAGCTT 439

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A.GeneSeq.101002 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CWN.1.1.353 @runat.03062003.085613.16797 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	661	83.6	236	23	AAU74297	Anti-human AILIM m
2	656.5	83.0	241	22	AA82912	Human immune respo
3	651	82.3	236	21	AA96297	Human IGFAM-9 immu
4	638	80.7	260	23	ABP41164	Human ovarian anti
5	637.5	80.6	237	21	AA96298	Human IGFAM-10 imm
6	634	80.6	246	22	AA899115	Human protein SEQ
7	633.5	80.1	237	21	AA96289	Human IGFAM-1 immu
8	632.5	80.0	234	14	AA838162	Sequence of the ka
9	629.5	79.6	234	13	AA820058	Light chain of 306
10	624.5	79.0	237	21	AA96301	Human IGFAM-13 imm
11	624.5	79.0	237	21	AA815546	Human immune syste
12	623	78.8	236	14	AA842065	Human anti-HBs lig
13	617	78.0	139	22	ABP43157	Human ovarian anti
14	609	77.0	224	22	AA875040	TRO005 HuMab kappa
15	606	76.6	224	22	AA875044	TRO005 HuMab kappa
16	604	76.4	236	21	AA96293	Human IGFAM-5 immu
17	592	74.8	234	18	AAW11638	Human anti-RSV mon
18	590	74.6	236	16	AA877614	Humanised SGI.1 VL
19	590	74.6	236	23	ABP51696	SGI.1 light chain
20	589	74.5	224	22	AA875043	TRO005 HuMab kappa
21	588	74.3	164	20	AA34317	IGG antibody 2.6.1
22	585.5	74.0	235	18	AAW11640	Human anti-RSV mon
23	584	73.8	235	21	AA803684	Immunoglobulin kap
24	579	73.2	129	21	AA55722	Amino acid sequenc
25	578	73.1	117	14	AA83851	Human V-kappa frag
26	578	73.1	117	15	AA862931	Human V-kappa vk65
27	578	73.1	117	17	AAW03949	DNA fragment vk65
28	578	73.1	117	18	AAW41147	Human vkappa65.15
29	578	73.1	117	19	AAW62185	Human DNA vkappa65
30	578	73.1	117	20	AA540432	Amino acid sequenc
31	577	72.9	130	21	AA556737	Amino acid sequenc
32	576	72.8	234	18	AAW10233	TF8-S69 CDR-grafce
33	576	72.8	236	21	AA96300	Human IGFAM-12 imm
34	574	72.6	214	20	AA908600	JP11127855 Seq ID
35	573	72.4	233	21	AA803713	Immunoglobulin kap
36	573	72.4	363	22	AAU14228	Human novel protei
37	572	72.3	124	21	AA556723	Amino acid sequenc
38	572	72.3	134	23	AAW47645	Human protein sequ
39	572	72.3	367	22	AAU14556	Human novel protei
40	571	72.2	132	18	AAW25841	Human anti-tumour
41	568	71.8	224	22	AA875041	TRO005 HuMab kappa
42	568	71.8	234	12	AA813050	CD4-specific CDR-g
43	567	71.7	129	23	ABG33326	Thrombopoietin ego
44	567	71.7	214	21	AA993735	The kappa chain of
45	566	71.6	129	16	AA865018	93KA9 anti-Varicel

# ALIGNMENTS

RESULT 1

AAU74297

ID AAU74297 standard; Protein; 236 AA.

XX

AC AAU74297;

XX

DT 12-MAR-2002 (first entry)

XX

DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.

XX

Human; antirheumatic; antiarthritis; antidiabetic; antipsoriatic;

antiallergic; antitumor; neuroprotective; antithyroid; vasotropic;

immunosuppressive; dermatological; antiinflammatory; hepatotropic;

activation inducible lymphocyte immunomodulatory molecule; AILIM;

monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;

multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;

allergic contact-type dermatitis; chronic inflammatory dermatosis;

systemic lupus erythematosus; autoimmune disorder; inflammation;

graft versus host reaction; immune rejection; intestinal immunity;





FT	Region	/note= "immunoglobulin domain motif"
FT	219..225	
FT	FT	/note= "Ig MHC motif"
FT	Region	197..240
FT	FT	/note= "immunoglobulin and MHC protein motif"
FT	Region	158..180
FT	FT	/note= "immunoglobulin and MHC protein motif"
FT	Region	219..236
FT	FT	/note= "immunoglobulin and MHC protein motif"
XX	XX	
PN	WO200168696-A1.	
PN	XX	
PD	20-SEP-2001.	
XX	XX	
PF	15-MAR-2001; 2001WO-US08518.	
XX	XX	
PR	15-MAR-2000; 2000US-189417P.	
XX	XX	
PA	(INCY-) INCYTE GENOMICS INC.	
XX	XX	
PI	Tang YT, Hillman JL, Baughn MR;	
XX	XX	
DR	WPI: 2001-590044/66.	
XX	N-PSDB; AAB26799.	
XX	XX	
PT	Novel human immune response proteins, for treating immunological disorders and cell proliferative disorders, and for assessing the effects of exogenous compounds on the expression of HIRP molecules	
PT	PT	
PT	PT	
PS	Claim 1; Page 85; 95pp; English.	
XX	XX	
CC	The invention is based on the discovery of new human immune response proteins (HIRP), the polynucleotides encoding them, and the use of these compositions for the diagnosis, treatment or prevention of immunological and cell proliferative disorders.	
CC	The present sequence is that of human immune response protein 1 (HIRP1, incyte ID No. 610031lCD1), as determined from a polynucleotide assembled e.g. from a lung adenocarcinoma cDNA library clone. The amino acid sequence shows homology, from residue W123 to C241, to an HIV-1 antigen binding protein, and further homologies suggest that it may be an immunoglobulin HIRP polynucleotides and polypeptides are useful for the diagnosis, treatment and prevention of cell proliferative disorders (e.g. cancers, arteriosclerosis, actinic keratosis, bursitis, mixed connective tissue disease (MCTD), myelofibrosis, psoriasis, leukaemia, hepatitis, cirrhosis and atherosclerosis), and immunological disorders e.g. AIDS, Addison's disease, adult respiratory distress syndrome (ARDS), anaemia, asthma, autoimmune diseases, contact dermatitis, diabetes mellitus, cholecystitis, Crohn's disease, atrophic gastritis, Goodpasture's syndrome, multiple sclerosis, irritable bowel syndrome, osteoporosis, rheumatoid arthritis, ulcerative colitis, trauma, and viral, bacterial, fungal, parasitic, protozoal and helminthic infections. The polypeptides are also used to screen for agonist and antagonist compounds of therapeutic use.	
XX	XX	
SQ	Sequence	241 AA;
Alignment Scores:		
Pred. No.:	3,978-60	Length: 241
Score:	656.50	Matches: 127
Percent Similarity:	90.67%	Conservative: 9
Best Local Similarity:	84.67%	Mismatches: 9
Query Match:	83.00%	Indels: 5
DB:	22	Gaps: 1
US-08-728-463B-208 (1-439) x AAB82912 (1-241)		
QY	1	ATGGACATGAGTTCCTCCGCTCAGCTCTCGGGCTCTGTGCTCTGTTCCAGGTGCC
Db	1	MetAspMetArgValProIalaGlnleuLeuGlyleuLeuLeuTrrLeuProGlyAla
QY	61	AGATGTGACATCCAGATGACCCAGGTCTCCATCCTCCTGCTGTGATCTGTAGGAGACAGA

PT protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders

Claim 1; Page 85; 105pp; English.

The present sequence is the human immunoglobulin superfamily protein IGFAW-9. Its gene was isolated from a cDNA library of breast tumour tissue. It is expressed in reproductive, gastrointestinal and immune and haematopoietic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are common. The diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anaemia, arteriosclerosis aethma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.

Sequence 236 AA;

**Alignment Scores:**

Pred. No.:	1.48e-59	Length:	236
Score:	651.00	Matches:	126
Percent Similarity:	91.72%	Conservative:	7
Local Similarity:	86.90%	Mismatches:	12
Query Match:	82.30%	Indels:	0
DB:	21	Gaps:	0

JS-08-728-463B-208 (1-439) x AAY96297 (1-236)

[illegible]

## RESULT 4

3P41164

ABP41164 standard; Protein; 260 AA.

ABP41164:

23-AUG-2002 (first entry)

22

Human ovarian antigen HRACW30, SEQ ID NO:2296.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 2012.

**Homo sapiens.**

WO200200677-A1

03-JAN-2002

07-JUN-2001; 2001WO-US18569.

07-JUN-2000; 2000US-209467P.

(HUMA-) HUMAN GENOME SCI INC.

**Birse CE, Rosen CA;**

WPI; 2002-147878/19.

N-PSDB; ABQ54241.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases-

Claim 11; SEQ ID No 2296; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors of the invention. The invention additionally relates to polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), and toxic disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders, and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may furthermore be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting or to prepare antibodies in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/pub/published/pct> sequences.

Sequence 260 AA;

Alignment Scores:

Pred. No.:	3,46e-58	Length:	260
Score:	638.00	Matches:	125
Percent Similarity:	89.66%	Conservative:	5



410 TACCGCCATCIGATGAA 435





FT Protein 23..237  
 FT /label= IGFAM-13  
 FT Domain 38..112  
 FT /label= Ig\_domain  
 FT Domain 150..219  
 FT /label= Ig\_domain  
 FT Domain 193..236  
 FT /label= Ig\_domain  
 XX  
 PN WO200029583-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 19-NOV-1999; 99WO-US27566.  
 XX  
 PR 19-NOV-1998; 99US-0113635.  
 PR 22-DEC-1998; 98US-0113635.  
 PR 07-APR-1999; 99US-0128194.  
 XX  
 PR  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
 PI Lu DAM, Lal P, Hillman JL, Yang J;  
 XX  
 DR WPI: 2000-387796/33.  
 DR N-PSDB; AAA27393.  
 XX  
 XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
 PT protein is useful for preventing and treating disorders associated with  
 PT altered levels of the protein such as cancer, immune system disorders  
 PT  
 PS Claim 1; Page 87-88; 105pp; English.  
 XX  
 XX The present sequence is the human immunoglobulin superfamily protein  
 CC IGFAM-13. Its gene was isolated from a cDNA library of lung tumour  
 CC tissue. It is expressed in reproductive, gastrointestinal and  
 CC cardiovascular tissue, where cancer and inflammation are common. The  
 CC gene, protein, its antibodies, agonists and antagonists are suitable for  
 CC diagnosing and treating many diseases, including cancer, immune system  
 CC disorders (such as inflammation, AIDS, allergies, anaemia,  
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's  
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
 CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
 CC systemic lupus erythematosus and ulcerative colitis), complications of  
 CC cancer, haemodialysis and extracorporeal circulation, trauma and  
 CC haematopoietic cancer (such as leukaemia) and infections caused by  
 CC bacteria, viruses, fungi or parasites.  
 XX  
 SQ Sequence 237 AA;  
 Alignment Scores:  
 Pred. No.: 2 63e-57 Length: 237  
 Score: 629.50 Matches: 124  
 Percent Similarity: 91.78% Conservative: 10  
 Best Local Similarity: 84.93% Mismatches: 11  
 Query Match: 79.58% Indels: 1  
 DB: 21 Gaps: 1  
 US-08-728-463B-208 (1-439) x AAY96301 (1-237)  
 QY 1 ATGGACATGGAGTTCCCGTCTCAGCTCTCGGGGCTCCTGCTGCTGTGTTCCAGGTGCC 60  
 Db 1 MetAspMetArgValProAlaGlnLeuLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAla 20  
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 Db 21 ArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArg 40  
 QY 121 GTCCACATCATCTGTGCGGCGAGTACAGGTATTAGCAGCTGTTAGCTGGTATCAGCAG 180  
 Db 41 ValThrMetThrCysArgAlaSerGlnSerIleSerThrThrLeuAsnTrpThrGlnGln 60

QY 181 AAACCAGAGAAAGCCCTAAGTCCCTGATCTATCTGTCATCCAGTTTCGAAAGTGGGTC 240  
 Db 61 LysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80  
 QY 241 CCATCAAGGTTTCAGCGGCGAGTGGATCTCGGACAGATTTTCACTCTCCATCAGCAGCCTG 300  
 Db 81 ProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
 QY 301 CAGCCTGAAGATTTTGCACCTATTACTGCGCAACAG---TATGATAGTTTACCCGTACACT 357  
 Db 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerPheAsnThrHisMetTyrThr 120  
 QY 358 TTGGCCAGGGGACCAAGCTGGAGATCAACGAACTGTGGCTGCACCATCTCTCTTCATC 417  
 Db 121 PheGlyGlnGlyThrArgLeuGluMetLysArgThrValAlaAlaProSerValPheIle 140  
 QY 418 TTCCCGCCATCTGATGAA 435  
 Db 141 PheProProSerAspGlu 146  
 RESULT 11  
 AAB15546  
 ID AAB15546 standard; Protein; 237 AA.  
 XX  
 AC AAB15546;  
 XX  
 DT 28-FEB-2001 (first entry)  
 DE Human immune system molecule from Incyte clone 1666486.  
 KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;  
 KW antiarteriosclerotic; antidiabetic; antidiabetic; nephrotropic; cancer;  
 KW antigout; dermatological; antithyroid; virucide; hepatotropic; antibody;  
 KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;  
 KW gene therapy; diagnostic; immunological disorder; viral infection;  
 KW bacterial infection; fungal infection; parasitic infection; immunogen.  
 XX Homo sapiens.  
 PN WO200060080-A2.  
 PD 12-OCT-2000.  
 PF 04-APR-2000; 2000WO-US09072.  
 PR 05-APR-1999; 99US-0127852.  
 PR 05-MAY-1999; 99US-0132647.  
 XX (INCY-) INCYTE PHARM INC.  
 PI Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;  
 DR WPI: 2000-665005/64.  
 DR N-PSDB; AAA95785.  
 XX  
 PT New human immune system molecules 1-15 and polynucleotides encoding  
 PT them useful for diagnosing, treating or preventing e.g. immunological  
 PT disorders, infections, cell proliferative disorders, microbial  
 PT infections -  
 PS Claim 1; Page 83-84; 95pp; English.  
 XX  
 XX This sequence represents a human immune system molecule (IMOL) encoded  
 CC by the cDNA isolated as clone 1666486 from the Incyte BMAR0703 library.  
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
 CC (AAA95775-A95789), and compositions comprising them are useful for the  
 CC diagnosis, treatment or prevention of immunological disorders,  
 CC infections and cell proliferative disorders, including cancer. The IMOL  
 CC may be used to treat or prevent disorders associated with decreased  
 CC expression or activity of IMOL, such as immunological disorders  
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,  
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,





XX WPI; 2001-335567/35.  
XX Producing a human antibody phage display library comprises providing a  
XX transgenic animal whose genome comprises human immunoglobulin genes and  
XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
XX Example 37; Page 121-122; 161pp; English.  
XX The present invention describes a method (M1) for producing a human  
XX antibody phage display library (I), comprising: (1) providing a nonhuman  
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;  
XX (2) isolating nucleic acids encoding human antibody chains (III) from  
XX lymphatic cells; and (3) forming a library of display packages whose  
XX members comprise a nucleic acid encoding (III) which is displayed from  
XX the package. The method is used for producing a human antibody display  
XX library, e.g., a Fab phage display library. The display method may be  
XX used to screen nucleic acids encoding antibody chains obtained from  
XX immunised nonhuman transgenic animals, and from this a population of  
XX antibodies may be prepared. Production of a human monoclonal antibodies  
XX display library using this method means there is no need to immunise  
XX humans with antigens, and the difficulties faced with immortalising B  
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
XX represent sequences used in the exemplification of the present invention.

SQ Sequence 224 AA;

#### Alignment Scores:

Pred. No.:	3 61e-55	Length:	224
Score:	609.00	Matches:	116
Percent Similarity:	99.19%	Conservative:	6
Best Local Similarity:	94.31%	Mismatches:	1
Query Match:	76.99%	Indels:	0
DB:	22	Gaps:	0

US-08-728-463B-208 (1-439) x AAB75040 (1-224)

QY	67	GACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGTAGGACAGAGTCACC	126
DB	1	AsnileGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr	20
QY	127	ATCATTGTCGGCGAGTCAGGATTTAGCAGCTGTAGCTGTAGCTATCAGCAGAACCA	186
DB	21	IleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysPro	40
QY	187	GAGAAAGCCCTAAGTCCCTGATCTATCTGCTATCCAGTTTGCAGTGGGGTCCCATCA	246
DB	41	GlulysAlaProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer	60
QY	247	AGTTTCAGCGGCGAGTGGATCTGGACAGATTTCCATCTCACCATCAGACGCTGCAGCTT	306
DB	61	ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80
QY	307	GAAGATTTCGAATTTACTTACCTGCCAACAGTATGATGTTACCGTACACTTTTGGCCAG	366
DB	81	GlusppheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProPheThrPheGlyPro	100
QY	367	GGGACCAAGCTGGAGATCAACAGAACTGTGGCTGCACCATCTCTCTTCTTCCCGCCA	426
DB	101	GlyThrLysValAspIleLysArgThrValAlaAlaProSerValPheIlePheProPro	120
QY	427	TCTGATGAA	435
DB	121	SerAspGlu	123

#### RESULT 15

AAB75044

ID AAB75044 standard; Protein; 224 AA.

XX

AC AAB75044;

XX

DT 19-JUL-2001 (first entry)

XX

DE TRO005 HuMab kappa chain protein sequence 359K.  
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
XX human antibody phage display library; immunisation; transgenic animal.  
XX Homo sapiens.  
XX Synthetic.  
XX WO200125492-A1.  
XX 12-APR-2001.  
XX 02-OCT-2000; 2000WO-US27237.  
XX 02-OCT-1999; 99US-0157415.  
XX 01-DEC-1999; 99US-0453234.  
XX (BIOS-) BIOSITE DIAGNOSTICS INC.  
XX (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.  
XX Buechler J, Valkirs G, Gray J, Lonberg N;  
XX WPI; 2001-335567/35.  
XX Producing a human antibody phage display library comprises providing a  
XX transgenic animal whose genome comprises human immunoglobulin genes and  
XX isolating nucleic acids encoding antibody chains from lymphatic cells -  
XX Example 37; Page 121-122; 161pp; English.  
XX The present invention describes a method (M1) for producing a human  
XX antibody phage display library (I), comprising: (1) providing a nonhuman  
XX transgenic animal (II) whose genome comprises human immunoglobulin genes;  
XX (2) isolating nucleic acids encoding human antibody chains (III) from  
XX lymphatic cells; and (3) forming a library of display packages whose  
XX members comprise a nucleic acid encoding (III) which is displayed from  
XX the package. The method is used for producing a human antibody display  
XX library, e.g., a Fab phage display library. The display method may be  
XX used to screen nucleic acids encoding antibody chains obtained from  
XX immunised nonhuman transgenic animals, and from this a population of  
XX antibodies may be prepared. Production of a human monoclonal antibodies  
XX display library using this method means there is no need to immunise  
XX humans with antigens, and the difficulties faced with immortalising B  
XX cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
XX represent sequences used in the exemplification of the present invention.

SQ Sequence 224 AA;

#### Alignment Scores:

Pred. No.:	7.43e-55	Length:	224
Score:	606.00	Matches:	116
Percent Similarity:	98.37%	Conservative:	5
Best Local Similarity:	94.31%	Mismatches:	2
Query Match:	76.61%	Indels:	0
DB:	22	Gaps:	0

US-08-728-463B-208 (1-439) x AAB75044 (1-224)

QY	67	GACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGTAGGACAGAGTCACC	126
DB	1	GlulysValMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr	20
QY	127	ATCATTGTCGGCGAGTCAGGATTTAGCAGCTGTAGCTGTAGCTATCAGCAGAACCA	186
DB	21	IleThrCysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysPro	40
QY	187	GAGAAAGCCCTAAGTCCCTGATCTATCTGCTATCCAGTTTGCAGTGGGGTCCCATCA	246
DB	41	GlulysAlaProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer	60
QY	247	AGTTTCAGCGGCGAGTGGATCTGGACAGATTTCTCTCACCATCAGACGCTGCAGCTT	306
DB	61	ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro	80



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QY 307 GAAGATTTGCAACTTATTACTGCCAACAGTATGATAGTTACCCGTACACTTTGGCCAG 366  
|||||  
Db 81 GluAspPheAlaThrTyTyTyCysGlnGlnTyAsnSerTyProIleThrPheGlyGln 100  
|||||  
QY 367 GGGACCAAGCTGGAGATCAACGAACTGTGGTGCACCATCTGTCTTCATCTTCCCGCCA 426  
|||||  
Db 101 GlyThrArgLeuGluIleLysArgThrValAlaAlaProSerValPheIlePheProPro 120  
|||||  
QY 427 TCTGATCAA 435  
|||||  
Db 121 SerAspGlu 123

Search completed: June 3, 2003, 09:02:23  
Job time : 30.5618 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 18.6255 Seconds

(without alignments)  
4764.744 Million cell updates/sec

Title: US-08-728-463B-208

Perfect score: 791

Sequence: 1 ATGGACATGGAGTTCCTCCGT.....CCCGCATCTGATGAAGCTT 439

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-O=/cgn2\_1/USPTO\_spool/US08728463/runat\_03062003\_085618\_16959/app.query.fasta\_1.3690  
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNIT8=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database :

Published Applications AA: \*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW PUB.pcp: \*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW PUB.pcp: \*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW PUB.pcp: \*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pcp: \*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW PUB.pcp: \*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp: \*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW PUB.pcp: \*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp: \*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW PUB.pcp: \*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pcp: \*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW PUB.pcp: \*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	661	83.6	236	10	US-09-859-053-30 Sequence 30, Appl
2	592	74.8	234	10	US-09-740-002-24 Sequence 24, Appl
3	590	74.6	236	9	US-10-006-593-69 Sequence 69, Appl
4	585.5	74.0	234	10	US-09-740-002-26 Sequence 26, Appl

5	567	71.7	214	9	US-10-153-382-19	Sequence 19, Appl
6	553	69.9	214	9	US-09-875-221A-128	Sequence 128, App
7	553	69.9	214	10	US-09-949-559-128	Sequence 128, App
8	553	69.9	237	9	US-10-020-786-10	Sequence 10, Appl
9	550	69.5	237	10	US-09-056-160B-100	Sequence 100, App
10	550	69.5	491	12	US-10-011-125-2	Sequence 2, Appl
11	546.5	69.1	235	10	US-09-800-729-152	Sequence 152, App
12	545	68.9	234	10	US-09-800-729-150	Sequence 150, App
13	540.5	68.3	211	10	US-09-974-449-36	Sequence 36, Appl
14	539	68.1	237	9	US-10-227-694-1	Sequence 1, Appl
15	539	68.1	237	10	US-09-940-166A-6	Sequence 6, Appl
16	538.5	68.1	235	10	US-09-910-059-52	Sequence 52, Appl
17	537	67.9	214	10	US-09-940-166A-2	Sequence 2, Appl
18	537	67.9	214	10	US-09-811-384-11	Sequence 11, Appl
19	537	67.9	218	9	US-09-925-179-9	Sequence 9, Appl
20	537	67.9	218	10	US-09-802-077-9	Sequence 9, Appl
21	537	67.9	218	10	US-09-802-096-9	Sequence 9, Appl
22	537	67.9	218	10	US-09-920-171-13	Sequence 13, Appl
23	536	67.8	218	10	US-09-917-410-2	Sequence 2, Appl
24	536	67.8	245	9	US-09-797-941A-6	Sequence 6, Appl
25	535	67.6	214	9	US-10-253-366-1	Sequence 1, Appl
26	535	67.6	237	9	US-10-020-786-8	Sequence 8, Appl
27	535	67.6	237	9	US-10-227-694-4	Sequence 4, Appl
28	533	67.4	139	9	US-10-153-382-31	Sequence 31, Appl
29	533	67.4	218	10	US-09-920-171-15	Sequence 15, Appl
30	533	67.4	218	10	US-09-920-171-17	Sequence 17, Appl
31	533	67.4	218	10	US-09-920-171-19	Sequence 19, Appl
32	533	67.4	218	10	US-09-920-171-24	Sequence 24, Appl
33	532.5	67.3	235	10	US-09-910-059-99	Sequence 99, Appl
34	529	66.9	239	10	US-09-825-012-9	Sequence 9, Appl
35	528	66.8	128	10	US-09-855-271-26	Sequence 26, Appl
36	528	66.8	218	9	US-09-925-179-67	Sequence 67, Appl
37	527	66.6	107	9	US-10-035-637-2	Sequence 2, Appl
38	522.5	66.1	235	10	US-09-910-059-97	Sequence 97, Appl
39	521	65.9	212	12	US-10-011-125-5	Sequence 5, Appl
40	519.5	65.7	235	9	US-10-153-382-7	Sequence 7, Appl
41	519	65.6	234	9	US-10-153-382-15	Sequence 15, Appl
42	518	65.5	224	9	US-09-453-234-48	Sequence 48, Appl
43	512.5	64.8	242	9	US-09-726-258-51	Sequence 51, Appl
44	512.5	64.8	242	9	US-09-726-258-56	Sequence 56, Appl
45	511.5	64.7	242	9	US-09-726-258-62	Sequence 62, Appl

#### ALIGNMENTS

RESULT 1  
US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tezuka, Takashi  
; APPLICANT: Hori, No. US20020102658A1uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30

Alignment Scores: 2.22e-51 Length: 236  
Pred. No.: 236





Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrProPheThrPheGlyPro 100  
QY 367 GGGACCAAGCTGGAGATCAAAACCACTGGCTGGCACCACCTCTTCTTCACTTCCGGCA 426  
Db 101 GlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPheIlePhePro 120  
QY 427 TCTGATGAA 435  
Db 121 SerAspGlu 123

## RESULT 6

US-09-875-221A-128  
; Sequence 128, Application US/09875221A  
; Publication No. US20030026805A1  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Brown, Derek Thomas  
; APPLICANT: Weir, Andrew Neil Charles  
; APPLICANT: Popplewell, Andrew George  
; APPLICANT: Chapman, Andrew Paul  
; APPLICANT: King, David John  
; TITLE OF INVENTION: Biological Products  
; FILE REFERENCE: Carp-0089  
; CURRENT APPLICATION NUMBER: US/09/875,221A  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: GB0013810.7  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 128  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Grafted light chain for fab and modified fab

US-09-875-221A-128

Alignment Scores:  
Pred. No.: 1,08e-41 Length: 214  
Score: 553.00 Matches: 107  
Percent Similarity: 92.68% Conservative: 7  
Best Local Similarity: 86.99% Mismatches: 9  
Query Match: 69.91% Indels: 0  
DB: Gaps: 0

US-08-728-463B-208 (1-439) x US-09-875-221A-128 (1-214)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCCTGCTGCTGCTAGGAGACAGATCACC 126  
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGGTGTAGCTGGTATCAGCAGAAACA 186  
Db 21 IleThrCysLysAlaSerGlnAsnValGlyThrAsnValAlaAlaTrpTyrGlnGlnLysPro 40  
QY 187 GAGAACCCCTTAAGTCCCTGATCTATTCTGCAATCCAGTTTGCAAGTGGGTCCCATCA 246  
Db 41 GlyLysAlaProLysAlaLeuIleTyrSerAlaSerPheLeuTyrSerGlyValProTyr 60  
QY 247 AGGTTCCAGCGCAGTCGATCGGACAGATTTCACTCTCACCATCAGCAGCTCGAGCCT 306  
Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
QY 307 GAAGATTTTGCACTTATTACTGCCAACAGATGATAGTTACCCGTACACTTTGGCCAG 366  
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnIleTyrProLeuThrPheGlyGln 100  
QY 367 GGGACCAAGCTGGAGATCAAAACCACTGGCTGGCACCACCTCTTCTTCACTTCCGGCA 426  
Db 101 GlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPheIlePhePro 120  
QY 427 TCTGATGAA 435

RESULT 8  
US-10-020-786-10  
; Sequence 10, Application US/10020786  
; Publication No. US20030073164A1

Db 121 SerAspGlu 123

## RESULT 7

US-09-949-559-128  
; Sequence 128, Application US/09949559  
; Patent No. US20020151682A1  
; GENERAL INFORMATION:  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Brown, Derek Thomas  
; APPLICANT: Weir, Andrew Neil Charles  
; APPLICANT: Popplewell, Andrew George  
; APPLICANT: Chapman, Andrew Paul  
; APPLICANT: King, David John  
; TITLE OF INVENTION: Biological Products  
; FILE REFERENCE: Carp-0095  
; CURRENT APPLICATION NUMBER: US/09/949,559  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 0013810.7GB  
; PRIOR FILING DATE: 2000-06-06  
; PRIOR APPLICATION NUMBER: 09/875,221  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 128  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Grafted light chain for fab and modified fab

US-09-949-559-128

Alignment Scores:  
Pred. No.: 1,08e-41 Length: 214  
Score: 553.00 Matches: 107  
Percent Similarity: 92.68% Conservative: 7  
Best Local Similarity: 86.99% Mismatches: 9  
Query Match: 69.91% Indels: 0  
DB: Gaps: 0

US-08-728-463B-208 (1-439) x US-09-949-559-128 (1-214)

QY 67 GACATCCAGATGACCCAGTCTCCATCTCCTGCTGCTGCTAGGAGACAGATCACC 126  
Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
QY 127 ATCACTTGTGGCGAGTCAGGTATTAGCAGCTGGTGTAGCTGGTATCAGCAGAAACA 186  
Db 21 IleThrCysLysAlaSerGlnAsnValGlyThrAsnValAlaAlaTrpTyrGlnGlnLysPro 40  
QY 187 GAGAACCCCTTAAGTCCCTGATCTATTCTGCAATCCAGTTTGCAAGTGGGTCCCATCA 246  
Db 41 GlyLysAlaProLysAlaLeuIleTyrSerAlaSerPheLeuTyrSerGlyValProTyr 60  
QY 247 AGGTTCCAGCGCAGTCGATCGGACAGATTTCACTCTCACCATCAGCAGCTCGAGCCT 306  
Db 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
QY 307 GAAGATTTTGCACTTATTACTGCCAACAGATGATAGTTACCCGTACACTTTGGCCAG 366  
Db 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnIleTyrProLeuThrPheGlyGln 100  
QY 367 GGGACCAAGCTGGAGATCAAAACCACTGGCTGGCACCACCTCTTCTTCACTTCCGGCA 426  
Db 101 GlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPheIlePhePro 120  
QY 427 TCTGATGAA 435  
Db 121 SerAspGlu 123

RESULT 8  
US-10-020-786-10  
; Sequence 10, Application US/10020786  
; Publication No. US20030073164A1



GENERAL INFORMATION:  
APPLICANT: Simmons, Laura C.  
APPLICANT: Klimowski, Laura  
APPLICANT: Reilly, Dorothea  
APPLICANT: Yaneura, Daniel G.  
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF  
FILE REFERENCE: P1793R1  
CURRENT APPLICATION NUMBER: US/10/020,786  
CURRENT FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: US 60/256,164  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 11  
SEQ ID NO 10  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: anti-VEGF light chain  
US-10-020-786-10

Alignment Scores:  
Pred. No.: 1.09e-41 Length: 237  
Score: 553.00 Matches: 108  
Percent Similarity: 90.48% Conservative: 6  
Best Local Similarity: 85.71% Mismatches: 12  
Query Match: 69.91% Indels: 0  
DB: 9 Gaps: 0

US-08-728-463B-208 (1-439) x US-10-020-786-10 (1-237)

QY 58 GCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGCTAGAGAC 117  
DB 21 AlaTyrAlaAspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAsp 40  
QY 118 AGAGTCACCATCACTTGTGCGGCGAGTTCAGGGTATTAGCAGCTGGTTCCTGGTATCAG 177  
DB 41 ArgValThrIleThrCysSerAlaSerGlnAspIleSerAsnTyrLeuAsnTrpTyrGln 60  
QY 178 CAGAAACACGAGAGAACCCCTTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAAGTGGG 237  
DB 61 GlnLysProGlyLysAlaProLysValLeuIleTyrPheThrSerSerLeuHisSerGly 80  
QY 238 GTCCCATCAAGTTTCAGCGGCGAGTTCGGACAGATTCACCTCTCACCATCAGCAGC 297  
DB 81 ValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSer 100  
QY 298 CTGCAGCCTGAAGATTTTGCACCTTATTACTGCAACAGTATGATGTTACCGTACACT 357  
DB 101 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrValProTrpThr 120  
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACAGAACTGTGGCTGCACCATCTCTCTTCATC 417  
DB 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIle 140  
QY 418 TTCCCGCCATCTGATGAA 435  
DB 141 PheProProSerAspGlu 146

RESULT 9  
US-09-056-160B-100  
Sequence 100, Application US/09056160B  
Patent No. US20020032315A1  
GENERAL INFORMATION:  
APPLICANT: Baca, Manuel  
APPLICANT: Wells, James A.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Lowman, Henry B.  
APPLICANT: Chen, Yvonne M.  
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES  
NUMBER OF SEQUENCES: 131  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,160B  
FILING DATE: 06-Apr-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/054,856  
FILING DATE: 06-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1093R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-056-160B-100

Alignment Scores:  
Pred. No.: 2.02e-41 Length: 237  
Score: 550.00 Matches: 107  
Percent Similarity: 90.48% Conservative: 7  
Best Local Similarity: 84.92% Mismatches: 12  
Query Match: 69.53% Indels: 0  
DB: 10 Gaps: 0

US-08-728-463B-208 (1-439) x US-09-056-160B-100 (1-237)

QY 58 GCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCTGCTGCTGCTAGAGAC 117  
DB 21 AlaTyrAlaAspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAsp 40  
QY 118 AGAGTCACCATCACTTGTGCGGCGAGTTCAGGGTATTAGCAGCTGGTTCCTGGTATCAG 177  
DB 41 ArgValThrIleThrCysSerAlaSerGlnAspIleSerAsnTyrLeuAsnTrpTyrGln 60  
QY 178 CAGAAACACGAGAGAACCCCTTAAGTCCCTGATCTATTCTGTCATCCAGTTTGCAAGTGGG 237  
DB 61 GlnLysProGlyLysAlaProLysValLeuIleTyrPheThrSerSerLeuHisSerGly 80  
QY 238 GTCCCATCAAGTTTCAGCGGCGAGTTCGGACAGATTCACCTCTCACCATCAGCAGC 297  
DB 81 ValProSerArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSer 100  
QY 298 CTGCAGCCTGAAGATTTTGCACCTTATTACTGCAACAGTATGATGTTACCGTACACT 357  
DB 101 LeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrValProTrpThr 120  
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACAGAACTGTGGCTGCACCATCTCTCTTCATC 417  
DB 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIle 140  
QY 418 TTCCCGCCATCTGATGAA 435  
DB 141 PheProProSerAspGlu 146

RESULT 10  
US-10-011-125-2  
Sequence 2, Application US/10011125  
Patent No. US20020142386A1  
GENERAL INFORMATION:

Alignment Scores:  
Pred. No.:

QY	76	ATGACCCAGTCTCCATCCTCACTCTGTGGCATCTGTAGGACAGAGTCACCACATTGT	139
Dd			
Dd	2	MetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThrIleThrCys	21
QY	136	CGGCGAGTCCAGGGTATTAGCAGCTGGTTAGCTTGCTGCCTCAGCAGAAAAACCAGAGAAAGCC	195
Dd			
Dd	22	ArgAlaSerGlnGlyIleAsnAsnTyrlauAlaTrpPheGlnGlnLysProGlyLysAla	41
QY	196	CCTAAGTCCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGGTGCCATCAAGGTTCCAGC	255
Dd			
Dd	42	ProLysSerLeuIleTyrlSerAlaSerIleLeuGlnSerGlyValProSerLysPheSer	61
QY	256	GSCAGTGGATCTGGGACAGATTTCACACTCACCATCAGCAGCCTGCAGACCTGAAGATTTT	315
Dd			
Dd	62	GlySerGlyserGlyThrAspPheThrLeuThrIleSerAsnLeuGlnProGluAspPhe	81
QY	316	GCAACTTATTACTGCCAACACATGATGATTACCCGTACACTTTTGGCCAGGGGACCAAG	375
Dd			
Dd	82	AlaThrTyrlTyrlCysGlnGlnTyrlAsnTyrlTyrlProLeuThrPheGlyGlyThrLys	101
QY	376	CTGGAGATCAACAGNACTGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGAA	435
Dd			
Dd	102	ValGluIleLys---ThrValAlaAlaProSerValPheIlePheProProSerAspGlu	120
<b>RESULT 14</b>			
<b>US-10-227-694-1</b>			
; Sequence 1, Application US/10227694			
; Publication NO. US20030077739A1			
<b>GENERAL INFORMATION:</b>			
; APPLICANT: Simmons, Laura			
; APPLICANT: Andersen, Dana			
; TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY			
; FILE REFERENCE: P1867RI			
; CURRENT APPLICATION NUMBER: US/10/227,694			
; PRIOR FILING DATE: 2002-08-26			
; PRIOR APPLICATION NUMBER: US 60/315,209			
; PRIOR FILING DATE: 2001-08-27			
; NUMBER OF SEQ ID NOS: 6			
; SEQ ID NO 1			
; LENGTH: 237			
; TYPE: PRF			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: Synthetic			
<b>US-10-227-694-1</b>			
<b>Alignment Scores:</b>			
Pred. No.:	1,96e-40	Length:	237
Score:	539.00	Matches:	106
Percent Similarity:	90.48%	Conservative:	8
Best Local Similarity:	84.13%	Mismatches:	12
Query Match:	68.14%	Indels:	0
DB:	9	Gaps:	0
<b>US-08-728-463B-208 (1-439) x US-10-227-694-1 (1-237)</b>			
QY	58	GCAGATGTGATCATCCAGATCACCAGTCTCCATCTCCTCACTGTGTCATCTGTAGGAGAC	117
Dd			
Dd	21	AlaTyrlAlaAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAsp	40
QY	118	AGAGTCACCATCACTTGTCTGGCGGAGTCAGGGTATTAGCAGCTGGTTAGCTGTGATCAG	177
Dd			
Dd	41	ArgValThrIleThrCysArgAlaSerGlnAspIleAsnAntyrlLeuAsnTrpTyrlGln	60
QY	178	CAGAAACCGAGAAAGCCCCTAAGTCCTGATCTATTCTGCATCCAGTTTGCAAAGTGGG	237
Dd			
Dd	61	GlnLysProGlyLysAlaProLysLeuLeuIleTyrlTyrlThrSerThrLeuHisSerGly	80
QY	238	GTCCCCATCAAGTTCCAGCGGAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGC	297
Dd			
Dd	81	ValProSerArgPheSerGlySerGlyThrAspTyrlThrLeuThrIleSerSer	100

QY 298 CTCGACGCTGAAGATTTCGCACTTATTACTGCGCAAGTATGATAGTATACCCGTACACT 357  
Db 101 LeuGlnProGluAspPhealaThrTyTCysGlnGlnGlyAsnThrLeuProProThr 120  
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACGAACTGGCTGGCCACCTCTCTTCATC 417  
Db 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheile 140  
QY 418 TTCCCGCCATCTGATGAA 435  
Db 141 PheProProSerAspGlu 146

## RESULT 15

US-09-940-166A-6

; Sequence 6, Application US/09940166A

; Patent No. US20020058324A1

; GENERAL INFORMATION:

; APPLICANT: Blank, Gregory S.

; Narindray, Daljit S.

; Zapata, Gerardo A.

; TITLE OF INVENTION: Protein Recovery

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinFatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/940.166A

; FILING DATE: 27-Aug-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/097,309

; FILING DATE: 13-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Schwartz, Timothy R.

; REGISTRATION NUMBER: 32171

; REFERENCE/DOCKET NUMBER: P1105R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-7467

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 237 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-940-166A-6

Alignment Scores:

Pred. No.:	1.96e-40	Length:	237
Score:	539.00	Matches:	106
Percent Similarity:	90.48%	Conservative:	8
Best Local Similarity:	84.13%	Mismatches:	12
Query Match:	68.14%	Indels:	0
DB:	10	Gaps:	0

US-08-728-463B-208 (1-439) x US-09-940-166A-6 (1-237)

QY 58 GCCAGATGTGACATCCAGATCCAGTCTCCATCTCTGTCGATCTGTAGGAGAC 117  
Db 21 AlaTyrAlaAspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAsp 40  
QY 118 AGAGTCACCATCACTTGTGGCGGAGTCAGGGTATTAGCAGCTGGTGTAGCCTGGTATCAG 177  
Db 41 ArgValThrIleThrCysArgAlaSerGlnAspIleAsnAsnTyrLeuAsnTrpTrGln 60

QY 178 CAGAAACCAGAGAAAGCCCTTAAGTCCCTCATCTATTCTGCATCCAGTTTGCAAAGTGGG 237  
Db 61 GlnLysProGlyLysAlaProLysLeuLeuIleTyrThrSerThrLeuHisSerGly 80  
QY 238 GTCCCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGC 297  
Db 81 ValProSerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSerSer 100  
QY 298 CTGACGCTGAAGATTTCGCACTTATTACTGCCCAACAGTATGATAGTATACCCGTACACT 357  
Db 101 LeuGlnProGluAspPhealaThrTyTCysGlnGlnGlyAsnThrLeuProProThr 120  
QY 358 TTGGCCAGGGACCAAGCTGGAGATCAACGAACTGGCTGGCCACCTCTCTTCATC 417  
Db 121 PheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheile 140  
QY 418 TTCCCGCCATCTGATGAA 435  
Db 141 PheProProSerAspGlu 146

Search completed: June 3, 2003, 09:51:20

Job time : 20.6525 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 9.99241 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

Title: US-08-728-463B-208  
Perfect score: 791  
Sequence: 1 ATGGACATGGAGTCCCGT.....CCGGCCATCTGATGAAGCTT 439

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO spool/US08728463/runat\_03062003\_085615\_16867/app\_query.fasta\_1.3690  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -MINLEN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CEN 1.1.97 @runat\_03062003\_085615\_16867 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	78.8	236	1	US-08-157-101A-5
2	584	73.8	235	3	US-08-812-586-16
3	578	73.1	117	4	US-09-042-353-48
4	578	73.1	117	4	US-08-758-417A-313
5	573	72.4	233	3	US-08-812-586-45
6	571	72.2	116	1	US-08-053-131-185
7	571	72.2	116	2	US-08-096-762-185
8	571	72.2	129	1	US-08-217-918-2
9	548.5	69.3	128	1	US-08-259-372A-14
10	548.5	69.3	128	1	US-08-468-671-14
11	542	68.5	233	2	US-07-934-373C-25
12	542	68.5	233	3	US-07-934-373C-25

13	542	68.5	233	4	US-08-146-206C-25
14	542	68.5	233	5	PCT-US93-07832-25
15	539.5	68.2	232	1	US-08-704-744-80
16	539	68.1	214	2	US-07-934-373C-39
17	539	68.1	214	3	US-08-437-642B-39
18	539	68.1	214	5	PCT-US93-07832-39
19	539	68.1	237	3	US-09-097-309-6
20	539	68.1	237	4	US-09-097-171A-10
21	539	68.1	237	4	US-09-422-712B-2
22	539	68.1	237	4	US-09-607-756-2
23	539	68.1	237	4	US-09-171-945-52
24	538.5	68.1	235	4	US-09-460-587-6
25	538	68.0	214	1	US-08-253-877C-5
26	538	68.0	214	2	US-08-452-164A-5
27	537	67.9	214	2	US-07-934-373C-40
28	537	67.9	214	2	US-08-788-800-11
29	537	67.9	214	3	US-08-437-642B-40
30	537	67.9	214	3	US-09-097-309-2
31	537	67.9	214	4	US-09-097-171A-2
32	537	67.9	214	4	US-09-460-587-2
33	537	67.9	214	5	PCT-US93-07832-40
34	537	67.9	218	2	US-08-887-352B-13
35	537	67.9	218	3	US-08-466-151-9
36	537	67.9	218	4	US-09-109-207C-13
37	537	67.9	218	4	US-09-296-005-13
38	537	67.9	218	4	US-08-466-163B-9
39	537	67.9	237	2	US-08-463-567A-25
40	537	67.9	237	2	US-08-463-667A-3
41	537	67.9	237	3	US-08-923-854-25
42	537	67.9	237	5	PCT-US91-09133-26
43	536	67.8	218	5	PCT-US96-13152-2
44	535	67.6	214	4	US-09-679-397-1
45	535	67.6	214	4	US-09-680-148-1

#### ALIGNMENTS

RESULT 1  
US-08-157-101A-5  
; Sequence 5, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944

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; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-5

Alignment Scores:
Pred. No.: 1-32e-63 Length: 236
Score: 623.00 Matches: 118
Percent Similarity: 90.34% Conservative: 13
Best Local Similarity: 81.38% Mismatches: 14
Query Match: 78.76% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-208 (1-439) x US-08-157-101A-5 (1-236)
QY 1 ATGGACATGGAGTCCCGTTCAGCTCCTGGGGCTCTGCTGCTGTTCCAGGTGCC 60
Db 1 MetaspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTppPheProGlyAla 20
QY 61 AGATGTGACATCCAGATGACCCAGCTCCATCCTCACTGCTGCTGCTAGGAGACAGA 120
Db 21 ArgCysAspIleGlnMetThrGlnSerProSerAlaMetAlaAlaSerValGlyAspArg 40
QY 121 GTCACCATCACTTGTCCGGCGAGTCAGGTTATTAGCAGCTGTTAGCTGTATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleGlyAsnTyrLeuValTppPheGlnGln 60
QY 181 AAACCCAGAGAAGCCCTTAAGTCCCTGATCTATCTGATCCAGTTCGAAAGTGGGTC 240
Db 61 LysProGlyLysValProLysArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyVal 80
QY 241 CCATCAAGTTTCAGCGGAGTGGATCGGACACATTTCACTCTCACCATCAGCAGCTG 300
Db 81 ProSerArgPheSerGlySerGlyThrGlyThrGlyThrLeuThrIleSerArgLeu 100
QY 301 CAGCTGAAGATTTTGAACCTTATTACTGCAACAGTATGATGATACCGTACACTTTT 360
Db 101 GlnProGluAspPheAlaThrTyrTyrCysLeuHisAsnTyrProLeuSerPhe 120
QY 361 GCGCAGGGGACCAAGCTGGAGATCAACAGCACTGTGGCTGCACCATCTGCTTCATCTTC 420
Db 121 GlyGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
QY 421 CCGCCATCTGATGAA 435
Db 141 ProProSerAspGlu 145

RESULT 2
US-08-812-586-16
; Sequence 16, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-16

Alignment Scores:
Pred. No.: 4.08e-59 Length: 235
Score: 584.00 Matches: 114
Percent Similarity: 85.52% Conservative: 10
Best Local Similarity: 78.62% Mismatches: 21
Query Match: 73.83% Indels: 0
DB: 3 Gaps: 0

US-08-728-463B-208 (1-439) x US-08-812-586-16 (1-235)
QY 1 ATGGACATGGAGTCCCGTTCAGCTCCTGGGGCTCTGCTGCTGTTCCAGGTGCC 60
Db 1 MetaspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTppPheProGlyAla 20
QY 61 AGATGTGACATCCAGATGACCCAGCTCCATCCTCACTGCTGCTGCTAGGAGACAGA 120
Db 21 ArgCysAlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArg 40
QY 121 GTCACCATCACTTGTCCGGCGAGTCAGGTTATTAGCAGCTGTTAGCTGTATCAGCAG 180
Db 41 ValThrIleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTppTyrGlnGln 60
QY 181 AAACCCAGAGAAGCCCTTAAGTCCCTGATCTATCTGCACTCCAGTTCGAAAGTGGGTC 240
Db 61 LysProGlyGlnAlaProArgLeuLeuIleTyrAspAlaSerSerArgAlaThrGlyIle 80
QY 241 CCATCAAGTTTCAGCGGAGTGGATCGGACAGATTTCACTCTCACCATCAGCAGCTG 300
Db 81 ProAspArgPheSerGlySerGlyThrGlyThrGlyThrLeuThrIleSerArgLeu 100
QY 301 CAGCTGAAGATTTTGAACCTTATTACTGCCACAGTATGATGATACCGTACACTTTT 360
Db 101 GluProGluAspPheAlaValTyrTyrGlyGlnGlnTyrGlySerSerProLeuThrPhe 120
QY 361 GCGCAGGGGACCAAGCTGGAGATCAACAGCACTGTGGCTGCACCATCTGCTTCATCTTC 420
Db 121 GlyGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPheIlePhe 140
QY 421 CCGCCATCTGATGAA 435
Db 141 ProProSerAspGlu 145

RESULT 3
US-09-042-353-48
; Sequence 48, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421

```



APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-0090300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 313:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 313:  
US-08-758-417A-313

Alignment Scores:		
Pred. No.:	1,61e-58	Length:
Score:	578.00	Matches:
Percent Similarity:	96.58%	Conservative:
Best Local Similarity:	94.87%	Mismatches:
Query Match:	73.07%	Indels:
DB:	4	Gaps:
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US-08-728-463B-208	(1-439)	x US-08-758-417A-313 (1-117)

[illegible]

RESULT 5  
 US-08-872-586-45  
 ; Sequence 45, Application US/08812586  
 ; Patent No. 6048704  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Martin  
 ; TITLE OF INVENTION: David Tilson  
 ; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
 ; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
 ; TITLE OF INVENTION:

NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,586  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/53862-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-812-586-45

Alignment Scores:	
Pred. No.:	7,526-58
Score:	573.00
Percent Similarity:	96.69%
Best Local Similarity:	90.91%
Query Match:	72.44%
DB:	3
	0
	0
Length:	233
Matches:	110
Conservative:	7
Mismatches:	4
Indels:	0
Gaps:	0

US-08-728-463B-208 (1-439) x US-08-812-586-45 (1-233)

Qy	73	CAGATGACCCAGTCTCCATCTCTCACTGCTGCATCTGTAGGAGACAGAGTCACCATCACT	132
Db	23	GluLeuThrGlnSerProSerValSerAlaSerValGlyAspArgValThrIleThr	42
Qy	133	TGTCGGGCAGTCAGGGTATTAGCAGCTGGTGGTACCTGGTATCAGCAGAAACACAGAGAA	192
Db	43	CysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLys	62
Qy	193	GCCCTTAAGTCCTCATCTATTCTGCATCCAGTTTGCAAGTGGGTGCCCATCAAGTTC	252
Db	63	AlaProLysLeuLeuIleTyrSerAlaSerSerLeuGlnSerGlyValProSerArgPhe	82
Qy	253	AGCGGAGTGGATCTGGGACAGATTCTCACTCTCACCATCAGACGCTCGAGCCTGAAGAT	312
Db	83	SerGlySerGlySerGlyThrAspPheSerLeuThrIleSerSerLeuGlnProGluAsp	102
Qy	313	TTTGGCACTTATTACTGCCAACAGATGATAGTATACCGTACACTTTTGGCCAGGGACC	372
Db	103	SerAlaThrTyrTyrCysGlnGlnAlaAsnSerPheProTyrThrPheGlyGlnGlyThr	122
Qy	373	AACTGTGAGATCAAAACGAACCTGTGGCTGACCACTCTGTCTTCATCTTCCCGGCATCTGAT	432
Db	123	LysValGluIleLysArgThrValAlaAlaProSerValPheIlePheProSerAsp	142
Qy	433	GAA	435
Db	143	Glu	143
Db			

RESULT 6  
US-08-053-131-185







Db 103 PheAlaThrTyrTyrCysGlnGlnAlaAspSerLeuProPheThrPheGlyGlyThr 122  
QY 373 AAGCTGAGATCAACGA 390  
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Db 123 LysValAspPheLysArg 128  
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RESULT 11  
US-07-934-373C-25  
; Sequence 25, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-25  
Alignment Scores:  
Pred. No.: 2,79e-54 Length: 233  
Score: 542.00 Matches: 106  
Percent Similarity: 89.76% Conservative: 8  
Best Local Similarity: 83.46% Mismatches: 13  
Query Match: 68.52% Indels: 0  
Gaps: 2  
US-08-728-463b-208 (1-439) x US-07-934-373C-25 (1-233)  
QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCTCATCTGCTGATCTGAGGA 114  
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Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35  
|||  
QY 115 GACAGATCCACCATCTGCTCGGGCAGTCAGGATATTAGCAGCTGGTTCCTGCTAT 174  
|||  
Db 36 AspArgValThrIleThrCysArgAlaSerGlnAspIleAsnAsnTyrLeuAsnTrpTyr 55  
|||  
QY '175 CACGAGAAACAGAGAAAGCCCTAAGTCCCTCATCTATTCTGATCCAGTTTGCAAGT 234  
|||  
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrThrSerThrLeuHisSer 75  
|||

QY 235 GGGTCCCATCAAGTTTCAGCGGAGTGGATCTGGACAGATTTTCACTCTCACCATCAGC 294  
|||  
Db 76 GlyValProSerArgPheSerGlySerGlyThrAspTyrThrLeuThrIleSer 95  
|||:|||||  
QY 295 AGCTTCGACGCTGAAGATTTTGCACCTATTACTGCAACAGTATGATAGTTTACCCGTAC 354  
|||  
Db 96 SerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnGlyAsnThrLeuProPro 115  
|||:|||||  
QY 355 ACTTTTGGCCAGGACCAAGCTGGAGATCAAACTGGTGGTGGACCATCTGCTTTC 414  
|||  
Db 116 ThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSerValPhe 135  
|||:|||||  
QY 415 ATCTTCCCGCCCATCTGATCAA 435  
|||  
Db 136 IlePheProProSerAspGlu 142  
|||  
RESULT 12  
US-08-437-642B-25  
; Sequence 25, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/437,642B  
; FILING DATE: 09-May-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/146206  
; FILING DATE: 17-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-437-642B-25  
Alignment Scores:  
Pred. No.: 2,79e-54 Length: 233  
Score: 542.00 Matches: 106  
Percent Similarity: 89.76% Conservative: 8  
Best Local Similarity: 83.46% Mismatches: 13  
Query Match: 68.52% Indels: 0

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,671
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/259,372
/ FILING DATE: 14-JUN-1994
/ APPLICATION NUMBER: US 07/538,796
/ FILING DATE: 15-JUN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/871,426
/ FILING DATE: 21-APR-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/676,036
/ FILING DATE: 27-MAR-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/538,796
/ FILING DATE: 15-JUN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/192,754
/ FILING DATE: 11-MAY-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 06/925,196
/ FILING DATE: 31-OCT-1986
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 06/904,517
/ FILING DATE: 05-SEP-1986
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 11823-50-7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 128 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-468-671-14

Alignment Scores:
Pred. No.: 4,138-55 Length: 128
Score: 548.50 Matches: 107
Percent Similarity: 92.06% Conservative: 9
Best Local Similarity: 84.92% Mismatches: 9
Query Match: 69.34% Indels: 1
DB: 1 Gaps: 1

US-08-728-4638-208 (1-439) x US-08-468-671-14 (1-128)

QY 16 CCGGTT---CAGCTCTGGGGCTCTGCTGCTGTGTTCCAGTGCCAGATGTGACATC 72
Db |||||
3 ProValAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIle 22
QY 73 CAGATGACCCAGTCTCCATCTCTACTGTGCTACTCTTAGAGACAGAGTCACCATCACT 132
Db |||||
23 GlnMetThrGlnSerProSerSerValSerAlaSerValGlyAspArgValThrValThr 42
QY 133 TGTCCGGCGAGTCAGGGTATTAGCAGCTGGTGTAGCTGGTATCAGCAGAAACCAGAGAA 192
Db |||||
43 CysArgAlaSerGlnGlyIleSerSerTrpLeuAlaTrpTrpGlnGlnLysProGlyLys 62
QY 193 GCCCTTAAGTCCCTGATCTATTCTGCATCCAGTTTGAAAGTGGGTGCCCATCAAGGTTTC 252
Db |||||
63 AlaProLysLeuLeuIleHisAlaAlaSerSerLeuGlnSerGlyValProSerArgpHe 82
QY 253 AGCGGCGAGTGGATCTGGGACAGAGATTTTCACTCTCACCATCAGCAGCCTGCAGCTGAGAT 312
Db |||||
83 IleGlySerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAlaGluAsp 102
QY 313 TTTCGAACTTATTACTGCCAACAGTATGATGTTACCCGTACACTTTTGGCCGGGGACC 372
Db |||||

```



```
;
;
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-25

Alignment Scores:
Pred. No.: 2,796-54 Length: 233
Score: 542.00 Matches: 106
Percent Similarity: 89.76% Conservative: 8
Best Local Similarity: 83.46% Mismatches: 13
Query Match: 68.52% Indels: 0
DB: 5 Gaps: 0

US-08-728-463B-208 (1-439) x PCT-US93-07832-25 (1-233)
QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGCTCCATCTCAGTCTGCTGCTAGTA 114
Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35
QY 115 GACAGAGTCACCATCACTTGTGGCGAGTCAGGTTATTAGCAGCTGGTTAGCTGTAT 174
Db 36 AspArgValThrIleThrCysArgAlaSerGlnAspIleAenAenTyLeuAenTyr 55
QY 175 CAGCAGAAACCCAGAGAAAGCCCTTAAGTCCTGATCTATTCTGATCCAGTTTGCAGT 234
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrThrSerThrLeuHisSer 75
QY 235 GGGTCCCATCAAGGTTTCAGCGGAGTCGATCTGGGACAGATTTCACTCTCACCATCAGC 294
Db 76 GlyValProSerArgPheSerGlySerGlySerGlyThrAspTyrThrLeuThrIleSer 95
QY 295 AGCTCGAGCCTGAAGATTTTGCACCTATTATCTGCTGCAACAGTATGATGTTACCCGTAC 354
Db 96 SerLeuGlnProGluAspPheAlaThrTyrCysGlnGlnGlyAsnThrLeuProPro 115
QY 355 ACTTTTGGCCAGGGACCAAGCTGGAGATCAAAAGCAACTGTGCTGCACCATCTGCTTC 414
Db 116 ThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPhe 135
QY 415 ATCTTCCCGCATCTGATGAA 435
Db 136 IlePheProProSerAspGlu 142

RESULT 15
US-08-704-744-80
; Sequence 80, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
```

```
;
;
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-80

Alignment Scores:
Pred. No.: 5,416-54 Length: 232
Score: 539.50 Matches: 108
Percent Similarity: 89.76% Conservative: 6
Best Local Similarity: 85.04% Mismatches: 12
Query Match: 68.20% Indels: 1
DB: 1 Gaps: 1

US-08-728-463B-208 (1-439) x US-08-704-744-80 (1-232)
QY 55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCAGTCTGCTGCTAGTA 114
Db 16 GlyValHisSerAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGly 35
QY 115 GACAGAGTCACCATCACTTGTGGCGAGTCAGGTTATTAGCAGCTGGTTAGCTGTAT 174
Db 36 AspArgValThrIleThrCysLysAlaSerGlnAsnIleTyrLysAsnLeuAlaTyr 55
QY 175 CAGCAGAAACCCAGAGAAAGCCCTTAAGTCCTGATCTATTCTGATCCAGTTTGCAGT 234
Db 56 GlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAsnAlaLysSerLeuGluThr 75
QY 235 GGGTCCCATCAAGTTCAGCGGAGTCAGGTCAGGTCAGGATTTCACTCTCACCATCAGC 294
Db 76 GlyValProSerArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 95
QY 295 AGCTCGAGCCTGAAGATTTTGCACCTATTATCTGCTGCAACAGTATGATGTTACCCGTAC 354
Db 96 SerLeuGlnProGluAspPheAlaThrTyrCysGlnGlnTyrSer---GlyTyr 114
QY 355 ACTTTTGGCCAGGGACCAAGCTGGAGATCAAAAGCAACTGTGCTGCACCATCTGCTTC 414
Db 115 ThrPheGlyGlnGlyThrLysValGluLeuLysArgThrValAlaAlaProSerValPhe 134
QY 415 ATCTTCCCGCATCTGATGAA 435
Db 135 IlePheProProSerAspGlu 141
```

Search completed: June 3, 2003, 09:47:31  
Job time : 12.9924 secs

GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 22.1646 Seconds  
(without alignments) 4545.477 Million cell updates/sec

Title: US-08-728-463B-219  
 Perfect score: 967  
 Sequence: 1 AAGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 200000000  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing first 45 summaries

Command line parameters:

```

-MODEL=frame_r_n2p_model -DEV=xlp
-Q/cgln2/US0728463/runat 03062003 085615 16827/app_query.fasta_1.3690
-DB=PIR_73 -QMT=fastan -SUFFIX=pr -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum2 -TRANS=human40.cdi -LIST=45
-DONALC=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08728463 @CGN 1 1 177 @runat 03062003 085615 16827 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEFTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOF=6
-FCGAEXT=7 -YGAPOF=10 -YGAPEXT=0 -DELOF=6 -DELEXT=7

```

Database : PIR 73:★

```
1: _pid: *
```

2: pir2:★

3: pir3:★

4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	679	70.2		140	2	A49045	Ig heavy chain v r
2	639.5	66.1		140	2	S78052	Ig heavy chain pre
3	608	62.9		220	2	A49446	Ig gamma-1 heavy c
4	604	62.5		231	2	B23746	Ig Fab region IV-J
5	603	62.4		140	2	I37782	Ig variable region
6	593.5	61.4		126	1	S47010	Ig heavy chain v4.
7	590	61.0		147	2	S13519	Ig heavy chain v r
8	581.5	60.1		137	2	S31676	Ig heavy chain v r
9	581.5	60.1		139	2	S31586	Ig heavy chain v r
10	579	59.9		143	2	B49028	Ig heavy chain v-I
11	578	59.8		155	2	S31511	Ig heavy chain - h
12	576	59.6		155	2	S31512	Ig heavy chain - h
13	573	59.3		139	2	S31696	Ig heavy chain v r
14	572	59.2		146	1	GLH02	Ig heavy chain pre

## ALIGNMENTS

## RESULT 1

A49045

Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text change 23-Jul-1999

C;Accession: A49045

R;Grillot-Courvalin, C.; Brou

Eur. J. Immunol. 22, 1781-1788

A;Title: An anti-B cell autoantibody from Wiskott-Aldri

A;Reference number: A49045; MUID:92324290; PMID:1623923

A;Accession: A49045

**A;Status: preliminary**

A;Molecule type: DNA

A;Residues: 1-140 &lt;GRI&gt;

A;Cross-references: GB:S39381; NID:g250899; PIDN:AAB2241.1; PID:g250900

A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBIIP:108089)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

**C;Keywords:** heterotetramer; immunoglobulin

F;34-116/Domain: immunoglobulin homology &lt;IMM&gt;

Alignment Scores:					
Pred. No.:	7.18e-50	Length:	140		
Score:	679..00	Matches:	129		
Percent Similarity:	93.57%	Conservative:	2		
Best Local Similarity:	92.14%	Mismatches:	3		
Query Match:	70.22%	Indels:	6		
DB:	2	Gaps:	1		
US-08-728-463B-219 (1-524) x A49045 (1-140)					
Qy	13	ATGAAACACTGTGGTCTTCCTCCTCGTGTCAGCTCCTAGATGGTCTGTCTCAG	72		
Db	1	MetLysHisLeuTrpPhePheLeuLeuValAlaAProArgTrpValLeuSerGln	20		
Qy	73	GTGCAGCTACAGCATGTGGGGCGCAGCATGTTGAAGCCCTTCGGAGACCCTGTCCCTCAC	132		
Db	21	ValGlnLeuGlnGInTrpGlyValAclyLeuLeuLysProSerGluThrLeuSerLeuThr	40		





Db 141 AlaLeuGlyCysLeuValLysAspTyrPheProGluPro 153

RESULT 4  
B23746  
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: B23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: B23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-231 <LEO>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:140-209/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.71e-43 Length: 231  
Score: 604.00 Matches: 118  
Percent Similarity: 83.23% Conservative: 11  
Best Local Similarity: 76.13% Mismatches: 20  
Query Match: 62.46% Indels: 6  
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x B23746 (1-231)

QY 73 GTGCAGCTACAGAGTGGGGCGGAGCTGTGAAGCTTCGGAGACCTGTCCCTCACC 132  
Db 1 ValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLeuPheSerGlnThrLeuSerLeuThr 20  
QY 133 TGGCGTCTGTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCACCA 192  
Db 21 GlyAlaValTyrGlyGlySerPheSerAspTyrTyrTrpSerTrpIleArgGlnProPro 40  
QY 193 GGTAAAGGCTGGAGTGGATGTGTGAATCAATCATAGTGGAGAACCACTACACCCG 252  
Db 41 GlyLysGlyLeuGlnTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsnPro 60  
QY 253 TCTCTCAAGAGTCGAGTCCCATATCAGTAGACACCTCCCAAGAACCACTCTCTCGAA 312  
Db 61 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 80  
QY 313 CTGAGCTCTGTGACCGCTGGGACACGCTGTGTATTACTGTCCGAGAGTAATT----- 366  
Db 81 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgProProHisAsp 100  
QY 367 -----AATTGGTTCGACCCCTTGGGGCCAGGAAACCTGTGTCACCGTCTCTCAGCC 417  
Db 101 ThrSerGlyHisTyrTrpAsnTyrTrpGlyGlnGlyThrLeuValThrValSerSerGly 120  
QY 418 TCACCAAGGGCCATCGCTTCCTCCCTGGCACCTCTCCCAAGACCACTCTGGG--- 474  
Db 121 SerAlaSerAlaProThrLeuPheProLeuValSerCysGluAsnSerProSerAspThr 140  
QY 475 GGCACAGCGCCCTGGGCTGCTGTGGTCAAGGACTACTTCCCGCAA 519  
Db 141 SerSerValAlaValGlyCysLeuAlaGlnAspPheLeuProAsp 155

RESULT 5  
I37782  
Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaison, C.; Chaetagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by H  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37782  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2.06e-43 Length: 140  
Score: 603.00 Matches: 119  
Percent Similarity: 87.86% Conservative: 4  
Best Local Similarity: 85.00% Mismatches: 11  
Query Match: 62.36% Indels: 6  
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x I37782 (1-140)

QY 13 ATGAACACCTGTGGTTCCTCTCTCTGGGAGCTCTAGATGGGTCTGTCTCAG 72  
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
QY 73 GTGCAGCTACAGAGTGGGGCGGAGCTGTGAAGCTTCGGAGACCTGTCTCCTCACC 132  
Db 21 ValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeuThr 40  
QY 133 TGGCGTCTGTATGGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCACCA 192  
Db 41 CysThrValSerGlyGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProPro 60  
QY 193 GGTAAAGGCTGGAGTGGATGTGTGAATCAATCATAGTGGAGAACCACTACACCCG 252  
Db 61 GlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrAsnPro 80  
QY 253 TCTCTCAAGAGTCGAGTCCCATATCAGTAGACACCTCCCAAGAACCACTCTCTCGAA 312  
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100  
QY 313 CTGAGCTCTGTGACCGCTGGGACACGCTGTGTATTACTGTCCGAGAGTAATT----- 366  
Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgHisAsnSerSer 120  
QY 367 AATTGG-----TTCGACCCCTTGGGGCCAGGAAACCTGTGTCACCGTCTCTCCTCA 414  
Db 121 SerTrpTyrGlyArgTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 140

RESULT 6  
S47010  
Ig heavy chain V4.21-UniqueD-J5 region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S47010  
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.  
submitted to the EMBL Data Library, July 1994  
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bi  
A:Reference number: S47009  
A:Accession: S47010  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-126 <MAH>  
A:Cross-references: EMBL:235492; NID:g517254; PIDN:CAA84625.1; PID:g517255  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.32e-42 Length: 126  
Score: 593.50 Matches: 113  
Percent Similarity: 89.68% Conservative: 0  
Best Local Similarity: 89.68% Mismatches: 2  
Query Match: 61.38% Indels: 11  
DB: 2 Gaps: 1

US-08-728-463B-219 (1-524) x S47010 (1-126)

QY 70 CAGGTGAGCTAGACAGAGTGGGGCAGGAGCTGTTGAAGCCTTCGAGACCCCTGCTCCTC 129  
 Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
 QY 130 ACCTGGGCTCTATAGTGTCTCTTCAGTGGTACTACTAGTGGAGCTGGATCGCCAGCCA 189  
 Db 21 ThrCysAlaValTrpGlyGlySerPheSerGlyTyrTrpSerTrpIleArgGlnPro 40  
 QY 190 CCAGGTAAGGCTTGGAGTGGATTGGTGAATCAATCATAGTGAAGCAGCACCACTACAC 249  
 Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTrpAsn 60  
 QY 250 CCCTCTCTCAAGAGTCAGTCACCATATCAGTAGACAGTCCTCAAGAACAGTTCTCTG 309  
 Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80  
 QY 310 AACTGAGCTCTGTGACCCCTCGGACACGGCTGTATTACTGTGCGAGA----- 360  
 Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGlyGlyGln 100  
 QY 361 -----GTAATTAAATTGGTTCGACCCCTTGGGGCCAGGGAACC 396  
 Db 101 CysProLysLysAlaSerCysTrpThrLysAsnTrpPheAspProTrpGlyGlnGlyThr 120  
 QY 397 CTGGTCACCGTCTCTCTCA 414  
 Db 121 LeuValThrValSerSer 126

## RESULT 7

ig heavy chain V region precursor - human  
 C:Species: Homo sapiens (man)  
 C>Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S13519  
 R:Montari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
 Nucleic Acids Res. 19, 673, 1991  
 A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
 A:Reference number: S13519; MUID:91187691; PMID:2011536  
 A:Accession: S13519  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-147 <MOR>  
 A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:41-125/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 2,62e-42 Length: 147  
 Score: 590.00 Matches: 116  
 Percent Similarity: 86.43% Conservative: 5  
 Best Local Similarity: 82.86% Mismatches: 13  
 Query Match: 61.01% Indels: 6  
 DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x S13519 (1-147)

QY 13 ATGAACACCTGTGGTTCCTCTCTCGTGGCAGCTCTAGATGGTCTCTGCTCAG 72  
 Db 8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 27  
 QY 73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGAGACCCCTGCTCCCTCACC 132  
 Db 28 LeuGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 47  
 QY 133 TGGCGTCTCATAGTGGTTCCTTC-----AGTGGTTACTACTGGAGCTGGATCGCCAG 186  
 Db 48 CysThrValSerGlyGlySerIleSerSerSerSerTrpTrpGlyTrpIleArgGln 67  
 QY 187 CCACCAAGGTAAAGGCTCGAGTGGATTGGTGAATCAATCATAGTGAAGCAGCACTAC 246  
 Db 68 ProProGlyLysGlyLeuGluTrpIleGlySerIleTyrTrpSerGlySerThrTrpTrp 87

QY 247 AACCCGTCTCTCAAGAGTCAGTCCATATCAGTAGACACGTCACCAAGAACCAAGTTCTCT 306  
 Db 88 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 107  
 QY 307 CTGAACCTGAGCTCTGTGACCGCTGGCGACACGGCTGTATTACTGTGCGAGAGTAATT 366  
 Db 108 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgProLeu 127  
 QY 367 AATTGG-----TTGACCCCTTGGGGCCAGGGAACCCCTGTGTACCCGTCTCTCA 414  
 Db 128 LeuTrpPheGlyGluLeuPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 147

## RESULT 8

ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31676  
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31676  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-137 <CUI>  
 A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-116/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.: 1,38e-41 Length: 137  
 Score: 581.50 Matches: 114  
 Percent Similarity: 86.86% Conservative: 5  
 Best Local Similarity: 83.21% Mismatches: 15  
 Query Match: 60.13% Indels: 3  
 DB: 2 Gaps: 1

US-08-728-463B-219 (1-524) x S31676 (1-137)

QY 13 ATGAACACCTGTGGTTCCTCTCTCGTGGCAGCTCTAGATGGTCTCTGCTCAG 72  
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 73 GTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGAGACCCCTGCTCCCTCACC 132  
 Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
 QY 133 TGCCTGTCTATAGTGGTTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCACCA 192  
 Db 41 CysThrValSerGlyGlySerIleSerSerTrpTrpSerTrpIleArgGlnProAla 60  
 QY 193 GGTAAAGGCTCGAGTGGATTGGTGAATCAATCATAGTGAAGCAGCACTACCAACCCG 252  
 Db 61 GlyLysGlyLeuGluTrpIleGlyArgIleTyrThrSerGlySerThrAsnTrpAsnPro 80  
 QY 253 TCTCTCAAGAGTCAGTCACCATATCAGTAGACACGTCGCAAGAACCAAGTTCTCTGAA 312  
 Db 81 SerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeuLys 100  
 QY 313 CTGAGCTCTGTGACCGCTGGGACACGGCTGTATTACTGTGCGAGA-----GTA 363  
 Db 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgAspAlaProLeu 120  
 QY 364 ATTAATTGGTTCGACCCCTTGGGGCCAGGGAACCCCTGTGTACCCGTCTCTCA 414  
 Db 121 MetTyrGlyMetAspValTrpGlyGlnGlyThrValThrValSerSer 137

## RESULT 9

ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)





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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 9.9393 Seconds  
(without alignments)  
4373.264 Million cell updates/sec

Title: US-08-728-463B-219  
Perfect score: 967  
Sequence: 1 AGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool/US08728463/runat\_03062003.085614.16804/app.query.fasta\_1.3690  
-DB=SwissProt 40 -OPMT=fastan -SUFFIX=rep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1.1.76 @runat\_03062003.085614.16804 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	59.2	146	1 HV21 HUMAN	P06331 homo sapien
2	402	41.6	129	1 HV2F HUMAN	P01824 homo sapien
3	396	41.0	117	1 HV2G HUMAN	P01825 homo sapien
4	393.5	40.7	137	1 HV46 MOUSE	P01822 mus musculus
5	370	38.3	116	1 HV60 MOUSE	P18531 mus musculus
6	358	37.0	144	1 HV43 MOUSE	P01819 mus musculus
7	354	36.6	113	1 HV47 MOUSE	P01823 mus musculus
8	343	35.5	116	1 HV61 MOUSE	P18532 mus musculus
9	336	34.7	135	1 HV02 XENLA	P20957 xenopus lae
10	326.5	33.8	117	1 HV62 MOUSE	P18533 mus musculus
11	326.5	33.8	119	1 HV38 MOUSE	P01808 mus musculus
12	326	33.7	138	1 HV48 MOUSE	P03980 mus musculus
13	322.5	33.4	139	1 HV07 MOUSE	P01751 mus musculus
14	321	33.2	117	1 HV41 MOUSE	P01811 mus musculus
15	318.5	32.9	147	1 HV2H HUMAN	P04438 homo sapien
16	317.5	32.8	119	1 HV37 MOUSE	P01807 mus musculus
17	316	32.7	115	1 HV44 MOUSE	P01820 mus musculus
18	314.5	32.5	119	1 HV40 MOUSE	P01810 mus musculus

19	311.5	32.2	136	1 HV01 XENLA	P20956 xenopus lae
20	311	32.2	142	1 HV01 RAT	P01805 rattus norv
21	308.5	31.9	137	1 HV11 MOUSE	P01755 mus musculu
22	308	31.9	118	1 HV39 MOUSE	P01809 mus musculu
23	305	31.5	117	1 HV12 MOUSE	P01756 mus musculu
24	304	31.4	116	1 HV45 MOUSE	P01821 mus musculu
25	303.5	31.4	120	1 HV50 MOUSE	P06329 mus musculu
26	300	31.0	117	1 HV13 MOUSE	P01757 mus musculu
27	298.5	30.9	114	1 HV3B HUMAN	P01763 homo sapien
28	296.5	30.7	122	1 HV3G HUMAN	P01768 homo sapien
29	294	30.4	121	1 HV01 MOUSE	P01745 mus musculu
30	293.5	30.4	118	1 HV51 MOUSE	P06330 mus musculu
31	290.5	30.0	117	1 HV04 MOUSE	P01748 mus musculu
32	288.5	29.8	120	1 HV2B HUMAN	P01815 homo sapien
33	288	29.8	122	1 HV3A HUMAN	P01762 homo sapien
34	288	29.8	117	1 HV42 MOUSE	P01812 mus musculu
35	288	29.8	123	1 HV25 MOUSE	P01794 mus musculu
36	287.5	29.7	116	1 HV36 MOUSE	P01806 mus musculu
37	287	29.7	115	1 HV3D HUMAN	P01765 homo sapien
38	287	29.7	116	1 HV05 CARAU	P19181 carassius a
39	287	29.7	140	1 HV02 MOUSE	P01746 mus musculu
40	286	29.6	119	1 HV31 HUMAN	P01770 homo sapien
41	285	29.5	121	1 HV3J HUMAN	P01771 homo sapien
42	284	29.4	117	1 HV17 MOUSE	P01786 mus musculu
43	282.5	29.2	122	1 HV20 MOUSE	P01789 mus musculu
44	281.5	29.1	117	1 HV09 MOUSE	P01753 mus musculu
45	281.5	29.1	117	1 HV3C HUMAN	P01764 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID HV21 HUMAN STANDARD; PRT; 146 AA.  
 AC P06331;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG heavy chain V-II region ARH-77 precursor.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85205332; PubMed=3922855;  
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
 repeat sequence in 5' flanking region.";  
 RL Gene 33:181-189(1985).  
 DR PIR; A02101; G1HUH2.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
 FT DOMAIN 20 117 V SEGMENT.  
 FT DOMAIN 118 127 D SEGMENT.  
 FT DOMAIN 128 146 J SEGMENT.  
 FT DISULFID 42 115 BY SIMILARITY.  
 FT NON\_TER 146 146  
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;  
 Alignment Scores:  
 Pred. No.: 1.88e-41 Length: 146  
 Score: 572.00 Matches: 114  
 Percent Similarity: 81.51% Conservative: 5  
 Best Local Similarity: 78.08% Mismatches: 15  
 Query Match: 59.15% Indels: 12  
 DB: 3

SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;







Best Local Similarity: 51.39% Mismatches: 38  
 Query Match: 37.02% Indels: 10  
 DB: 1 Gaps: 1

US-08-728-463B-219 (1-524) x HV43\_MOUSE (1-144)

QY 13 ATGAACACCTGGTCTCTCCCTCCCTGGTGGCAGCTCTAGATGGTCTGTCTCAG 72  
 DB 1 MetAlaValLeuAlaLeuLeuPheCysLeuAlaThrPheProSerCysIleLeuSerGln 20

QY 73 GTGCAGCTACAGCAGTGGGGCGCAGACTGTTGAAGCCTTCGGAGACCTCTCCCTCACC 132  
 DB 21 ValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThr 40

QY 133 TCGCGTCTATGCTGGTCTCTCAGTGTACTACTGAGCTGGATCCGCCAGCACCA 192  
 DB 41 CysThrValSerGlyPheSerLeuThrGlyTyrglyValAsnTrpValArgGlnProPro 60

QY 193 GGTAAAGGCTCGAGTGGATTGTTGAATCAATCATAGTGGAGCAGCACTACACCCG 252  
 DB 61 GlyLysGlyLeuGluTrpLeuGlyThrIleTrpGlyAsnGlySerThrAspTyrAsnSer 80

QY 253 TCTCTCAAGAGTCCAGTACCATATCAGTAGACACGCTCCAAAGAACCCAGTTCTCTGAAA 312  
 DB 81 ThrLeuLysSerArgLeuThrIleThrLysAspAsnSerLysSerGlnValPheLeuLys 100

QY 313 CTGAGCTCTGTACCGCTCGGACACGGCTGTGTATTACTGTGCGAGAGTAATAATGG 372  
 DB 101 MetAsnSerLeuGlnThrAspAspThrAlaAaGlyTyr-TyrCysAlaSerValSerIleTyr 120

QY 373 TTC-----GACCCTGGGGCAGGAAACCCCTGGTC 402  
 DB 121 TyrTyrGlyArgSerAspLysTyrPheThrLeuAspTyrTrpGlyGlnGlyThrSerVal 140

QY 403 ACCGCTCTCTCA 414  
 DB 141 ThrValSerSer 144

RESULT 7  
 HV47\_MOUSE  
 ID HV47\_MOUSE STANDARD; PRT; 113 AA.  
 AC P01823;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 36-60.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=84024551; PubMed=6414509;  
 RA Juszcak E.C., Margolles M.N.;  
 RT "Amino acid sequence of the heavy chain variable region from the A/J  
 mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
 idio type."  
 RL Biochemistry 22:4291-4296(1983).  
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE  
 CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND  
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF  
 CC STRAIN A/J MICE.  
 DR PIR; A02098; G2MS60.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Antiarsonate antibody.  
 FT NON\_TER 113 113  
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;

Alignment Scores: 8.1e-23 Length: 113  
 Pred. No.: 354.00 Matches: 70  
 Score: 78.26% Conservative: 20  
 Best Local Similarity: 60.87% Mismatches: 23  
 Query Match: 36.61% Indels: 2  
 DB: 1 Gaps: 1

US-08-728-463B-219 (1-524) x HV47\_MOUSE (1-113)

QY 70 CAGGTGCAGCTACAGCAGTGGGGCGCAGGAGCTGTTGAAGCCTTCGGAGACCTCTCCCTC 129  
 DB 1 GluValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnThrLeuSerLeu 20

QY 130 ACCTCGCTGTATGCTGGTCTCTCAGTGTACTACTGAGCTGGATCCGCCAGCACCA 189  
 DB 21 ThrCysSerValThrGlyAspSerIleThrSerAspTyrTrpAsnTrpIleArgLysPhe 40

QY 190 CCAGCTAAGGCTCGAGTGGATTGTTGAATCAATCATAGTGGAGCAGCACTACAC 249  
 DB 41 ProGlyAsnLysLeuGluHisMetGlyTyrIleSerTyrSerGlySerThrTyrTyrAsn 60

QY 250 CCGTCTCTCAAGAGTCCAGTACCATATCAGTAGACACGCTCCAAAGAACCCAGTTCTCTCG 309  
 DB 61 ProSerLeuLysSerArgLysSerIleThrArgAspThrSerLysAsnGlnTyrTyrLeu 80

QY 310 AAACCTGAGCTCTGTACCGCTCGGACACGGCTGTGTATTACTGTGCGAGAGTAATAAT 369  
 DB 81 GlnLeuAsnSerValThrSerGluAspThrAlaThrTyrTyrCysThrSerLeu----- 98

QY 370 TGGTTCGACCCCTGGGGCAGGAAACCCCTGGTCACCGTCTCTCA 414  
 DB 99 ArgPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 113

RESULT 8  
 HV61\_MOUSE  
 ID HV61\_MOUSE STANDARD; PRT; 116 AA.  
 AC P18532;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 1B43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response."  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.  
 CC PIR; JTO508; HVMS1B.  
 DR HSSP; P01825; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.  
 FT DOMAIN 19 48 FRAMEWORK-1  
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 54 67 FRAMEWORK-2.  
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 85 116 FRAMEWORK-3.  
 FT DISULFID 40 114 BY SIMILARITY.  
 FT NON\_TER 116 116  
 SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;





Score: 326.00 Matches: 66  
Percent Similarity: 67.16% Conservative: 24  
Best Local Similarity: 49.25% Mismatches: 40  
Query Match: 33.71% Indels: 4  
DB: 1 Gaps: 2

US-08-728-463B-219 (1-524) x HV48\_MOUSE (1-138)

QY 25 TGGTTCCTCTCCCTGCGGAGCTCCTAGATGGTCTCTCAGTGGAGCTACAG 84  
Db 5 TyrilleLeuPheLeuValAlaThrAlaThrAspValHisSerGlnValGlnLeuGln 24  
QY 85 CAGTGGGCGCAGACCTGTTGAAGCCTTCGAGACCTGTCCTCACCTGCGCTGTAT 144  
Db 25 GlnProGluGluLeuValValProGlyAlaSerValGlnLeuSerCysLysAlaSer 44  
QY 145 GGTGGTTCCTTCACTGTTACTACTGAGCTGATCCGACCCAGCAGCTAAGGCTG 204  
Db 45 GlyHisThrPheThrAsnTyrTrpIleHisTrpValLysGlnArgProGlyGlnGlyLeu 64  
QY 205 GAGTGGATGCTGAATCAAT---CATAGTGAAGCACCACCACTACAACCGCTCTCTCAAG 261  
Db 65 GluTrpIleGlyLeuLeuAsnProAsnAspGlyArgSerAsnTyrAsnGlnLysPheLys 84  
QY 262 AGTCGAGTCACCATATACAGTACACGCTCCAGAACCCAGTCTCTCTGAACTGAGCTCT 321  
Db 85 AsnLysAlaThrLeuThrValAspLysSerSerThrAlaTyrMetGlnLeuSerSer 104  
QY 322 GTGACCGCTGGCAGACCGCTGTATTACTGTGCGAGA-----GTAATTAATGG 372  
Db 105 LeuThrProGluGluPheAlaValTyrCysAlaArgSerAspGlyTyrTyrAspTrp 124  
QY 373 TTCGACCCCTGGGCGCAGGACCTGTCACCGCTCTCTCA 414  
Db 125 PheValTyrTrpGlyGlnGlyThrLeuValThrPheSerAla 138

RESULT 13  
HV07\_MOUSE  
ID HV07\_MOUSE STANDARD; PRT; 139 AA.  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain v region B1-8/186-2 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J00529; AAA38170.1; -  
CC PIR: A02034; MHMS18.  
CC HSP: P01810; 2PBJ.  
DR InterPro:IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1...  
DR SMART: SM00406; IGV; 1:  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Alignment Scores:  
Pred. No.: 4,06e-20 Length: 139  
Score: 322.50 Matches: 65  
Percent Similarity: 67.42% Conservative: 24  
Best Local Similarity: 49.24% Mismatches: 38  
Query Match: 33.35% Indels: 5  
DB: 1 Gaps: 2

US-08-728-463B-219 (1-524) x HV07\_MOUSE (1-139)

QY 34 CTCCTCTCTGTCGAGCTCCTAGATGGTCTCTCAGTGGAGCTACAGCAGTGGGCG 93  
Db 8 LeuPheLeuAlaThrAlaThrGlyValHisSerGlnValGlnLeuGlnProGly 27  
QY 94 CGAGGACTGTTCAAGCCTTCGAGACCTGTCCTCACCTGCGCTGTCTATGGTGGTTC 153  
Db 28 AlaGluLeuValValProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47  
QY 154 TTCAGTGTGTACTACTGGAGCTGGATCGCGCAGCCAGCCAGCTAAGGCTCTGAGTGGATT 213  
Db 48 PheThrSerTyrTrpMetHisTrpValLysGlnArgProGlyArgGlyLeuGluTrpIle 67  
QY 214 GGTGAATCAAT---CATAGTGAAGCACCACCACTACAACCGCTCTCTCAAGTGGAGTC 270  
Db 68 GlyArgIleAspProAsnSerGlyGlyThrLysTyrAsnGlnLysPheLysSerLysAla 87  
QY 271 ACCATATCAGTAGACACGCTCCCAAGAACCCAGTCTCTCTGAAACTGAGCTCTGTGACCGCT 330  
Db 88 ThrLeuThrValAspLysProSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSer 107  
QY 331 CGGACACCGCTGTATTACTGTGCGAGAGTA-----ATTAATTTGGTTCGAC 378  
Db 108 GluAspSerAlaValTyrTyrCysAlaArgTyrAspTyrTyrGlySerSerTyrPheAsp 127  
QY 379 CCTTGGGCGCAGGAGCCTCGTCCACCGCTCTCTCA 414  
Db 128 TyrTrpGlyGlnGlyThrThrLeuThrValSerSer 139

RESULT 14  
HV41\_MOUSE  
ID HV41\_MOUSE STANDARD; PRT; 117 AA.  
AC P01811;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig heavy chain v region UPC10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83021113; PubMed=6181731;  
RA Auffray C., Sikorav J.L., Oillo R., Rougeon F.;  
RT "Correlation between D region structure and antigen-binding  
RT specificity: evidences from the comparison of closely related

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 46.5159 Seconds  
(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-219  
Perfect score: 967  
Sequence: 1 AGCTTGCCACCATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp  
-Q/cgn2 1/USPTO spool/US08728463/runat\_03062003 085614 16815/app query.fasta\_1.3690  
-DB=SPTREMBL 21 -OPMT=fastan -SURF=rspt -MINMATCH=0 1 -LOOPCT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1 1 380 @runat\_03062003 085614 16815 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTREMBL 21:.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archesp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	716.5	74.1	588	4	Q8WUX4	Q8wux4 homo sapien

ID	Q8WUX4	PRELIMINARY;	PRT;	588 AA.
2	716.5	74.1	597	4
3	716.5	74.1	618	4
4	710.5	73.5	597	4
5	655.5	67.8	473	4
6	641	66.3	613	4
7	590	61.0	496	4
8	583.5	60.3	150	4
9	504.5	52.2	471	4
10	496	51.3	479	11
11	491	50.8	119	4
12	449	46.4	278	11
13	441.5	45.7	473	11
14	421	43.5	468	11
15	420	43.4	168	11
16	419.5	43.4	463	11
17	416	43.0	482	11
18	412	42.6	613	11
19	407.5	42.1	147	4
20	399.5	41.3	473	11
21	399.5	41.3	473	11
22	398	41.2	469	11
23	394	40.7	613	4
24	387.5	40.1	437	11
25	380.5	39.3	597	4
26	380	39.3	494	4
27	378	39.1	474	11
28	372.5	38.5	497	4
29	371	38.4	488	11
30	367.5	38.0	489	11
31	363.5	37.6	122	4
32	363	37.5	487	11
33	363	37.5	573	4
34	359.5	37.2	480	11
35	358	37.0	481	11
36	355.5	36.8	484	11
37	355.5	36.8	486	11
38	355.5	36.8	614	4
39	354.5	36.7	481	11
40	353.5	36.6	298	11
41	351	36.3	140	11
42	351	36.3	496	4
43	350.5	36.2	479	11
44	343.5	35.5	484	11
45	342.5	35.4	481	11

#### ALIGNMENTS

RESULT 1

ID	Q8WUX4	PRELIMINARY;	PRT;	588 AA.
AC	Q8WUX4;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Hypothetical 64.4 kDa protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
RA	Strausberg R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC019235; AAH19235.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR003597; IG.c1.			
DR	InterPro; IPR003006; IG.MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; ig; 5.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGc1; 4.			

DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig; 5.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00407; IGc1; 4.	
DR	SMART; SM00406; IGV; 1.	
DR	SMART; SM00410; IG-like; 1.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.	
KW	Hypothetical protein.	
SEQ	SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;	

  

Alignment Scores:	
Pred. No.:	5,79e-63
Score:	716.50
Percent Similarity:	80.56%
Best Local Similarity:	76.67%
Query Match:	74.10%
DB:	4

  

US-08-728-463B-219 (1-524) x Q9BU10 (1-597)	
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QY	13	ATGAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCTCAGTA	
Db	1	MetIyShisLeuTPhPheLeuLeuLeuValAlaAlaProArg	
QY	73	GTGCAGCTACAGCAGTGGGGCGGAGGACTGTTGAAGCCTTCGGAGAG	
Db	21	ValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGlu	
QY	133	TGCGCTGCTATGGTGGTTCCTTCAGTGGTACTACTGGAGCTGGG	
Db	41	CysGlyValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrp	
QY	193	GCTAAGGGCTGAGAGTGGATGTGTGAATCAATCATAGTGGAGCG	
Db	61	GlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySer	
QY	253	TCTCTCAAGAGTCGAGTCACCATATCATAGTAGACACGTCCAAGAC	
Db	81	SerLeuLysSerArgValThrIleSerValAspThrSerLysLys	
QY	313	CTGAGCTCTGTGACCGCTCGGACACGGCTGTGTATTACTGTGCGG	
Db	101	LeuSerSerValAsnAlaAlaAspThrAlaValTyrTyrCysAla	
QY	370	-----TGGTTTCGACCCCTTGGGGCC	
Db	121	AlaSerProGlyThrAspGlyArgTyrGlyMetAspValTrpGlyG	
QY	403	ACGCTCTCTCAGCCTCAACCAAGGGCCCATCGGTCTTCCCTCGG	
Db	141	ThrValSerSerGlySerAlaSerAlaProThrLeuPheProLeu	
QY	463	AGCACTCTTGGG---GGCACAGCGCCCTGGGCTGCCTGGTCAAGG	
Db	161	SerProSerAspThrSerSerValAlaValGlyCysLeuAlaGlnA	

  

RESULT 3	
Q96AA6	
ID	Q96AA6
AC	PRELIMINARY; PRT; 618 AA.
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Hypothetical 67.8 kDa protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hu
OX	NCBI_TaxId=9606;
RP	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=LYMPH;
RA	Strausberg R.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017356; AH017356.1; -  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 5.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C69E0A6 CRC64;

Alignment Scores:  
Pred. No.: 5,83e-63 Length: 618  
Score: 716.50 Matches: 138  
Percent Similarity: 80.56% Conservative: 7  
Best Local Similarity: 76.67% Mismatches: 24  
Query Match: 74.10% Indels: 11  
DB: 4 Gaps: 2

US-08-728-463B-219 (1-524) x Q96AA6 (1-618)

```
QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
D 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 73 GTCAGCTACAGTGGGGCGGAGGACTCTTGAAGCTTCGAGACCCCTGCTCCCTCACC 132
D 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLeuLeuProSerGluThrLeuSerLeuThr 40
QY 133 TGGCGTCTCTATGGTGGTTCCTCTCAGTGGTTCCTCTCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 192
D 41 CysGlyValTrpGlyGlySerPheSerGlyTyrTrpSerTrpLeuArgGlnProPro 60
QY 193 GGTAAAGGCTGAGTGGATGTGGAATCAATCATAGTGGAGCAACCACTCAACCCG 252
D 61 GlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTyrAsnPro 80
QY 253 TCTCTCAAGAGTCAGTCCACCATATCAGTAGACACGTCGAGACCAAGTCTCTCTGAAA 312
D 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysGlnLeuSerLeuLys 100
QY 313 CTGAGCTCTGTGACCGCTGGCGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT 369
D 101 LeuSerSerValAsnAlaAlaAspThrAlaValTyrCysAlaArgValIleThrArg 120
QY 370 -----TGGTTCGACCTTTGGGCGGAGGAACTTGTCTCAG 402
D 121 AlaSerProGlyThrAspGlyArgTyrGlyMetAspValTrpGlyGlnGlyThrVal 140
QY 403 ACCGTCTCTCAGCTCAACCAAGGCCCATCGTCTTCCCTCTGGCACCCTCTCTCAAG 462
D 141 ThrValSerSerGlySerAlaSerAlaProThrLeuPheProLeuValSerCysGluAsn 160
QY 463 AGCACCTCTGGG---GGCACAGCGGCTGGCTGTGTCTGCTCAAGGACTACTTCCCGAA 519
D 161 SerProSerAspThrSerSerValAlaValGlyCysLeuAlaGlnAspPheLeuProAsp 180
```

## RESULT 4

Q9BQB8 PRELIMINARY; PRT; 597 AA.  
AC Q9BQB8  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Unknown (protein for MGC:1905) [protein for MGC:1228].  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MUSCLE;  
RA Strausberg R.;  
SQ Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -  
DR InterPro; IPR003599; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG; 5.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IG; 1.  
DR SMART; SM00410; IG like; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Alignment Scores:  
Pred. No.: 2.3e-62 Length: 597  
Score: 710.50 Matches: 137  
Percent Similarity: 80.00% Conservative: 7  
Best Local Similarity: 76.11% Mismatches: 25  
Query Match: 73.47% Indels: 11  
DB: 4 Gaps: 2

US-08-728-463B-219 (1-524) x Q9BQB8 (1-597)

```
QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 72
D 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 73 GTCAGCTACAGTGGGGCGGAGGACTGTGGAAGCTTCGAGACCCCTGCTCCCTCACC 132
D 21 ValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeuThr 40
QY 133 TGGCGTCTCTATGGTGGTTCCTCTCAGTGGTTCCTCTCTGGTGGCAGCTCCTAGATGGGTCTGTCTCAG 192
D 41 CysGlyValTrpGlyGlySerPheSerGlyTyrTrpSerTrpLeuArgGlnProPro 60
QY 193 GGTAAAGGCTGAGTGGATGTGGAATCAATCATAGTGGAGCAACCACTCAACCCG 252
D 61 GlyLysGlyLeuGluTrpIleGlyGluLeuAsnHisSerGlySerThrAsnTyrAsnPro 80
QY 253 TCTCTCAAGAGTCAGTCCACCATATCAGTAGACACGTCGAGACCAAGTCTCTCTGAAA 312
D 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysGlnLeuSerLeuLys 100
QY 313 CTGAGCTCTGTGACCGCTGGCGACACGGCTGTGTATTACTGTGCGAGAGTAATTAAT 369
D 101 LeuSerSerValAsnAlaAlaAspThrAlaValTyrCysAlaArgValIleThrArg 120
QY 370 -----TGGTTCGACCTTTGGGCGGAGGAACTTGTCTCAG 402
D 121 AlaSerProGlyThrAspGlyArgTyrGlyMetAspValTrpGlyGlnGlyThrVal 140
QY 403 ACCGTCTCTCAGCTCAACCAAGGCCCATCGTCTTCCCTCTGGCACCCTCTCTCAAG 462
D 141 ThrValSerSerGlySerAlaSerAlaProThrLeuPheProLeuValSerCysGluAsn 160
QY 463 AGCACCTCTGGG---GGCACAGCGGCTGGCTGTGTCTGCTCAAGGACTACTTCCCGAA 519
D 161 SerProSerAspThrSerSerValAlaValGlyCysLeuAlaGlnAspPheLeuProAsp 180
```

## RESULT 5

Q8TC63 PRELIMINARY; PRT; 473 AA.  
AC Q8TC63  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)



RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC016369; AAH16369.1; --  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Alignment Scores:  
 Pred. No.: 2,496-50 Length: 496  
 Score: 590.00 Matches: 120  
 Percent Similarity: 74.16% Conservative: 12  
 Best Local Similarity: 67.42% Mismatches: 36  
 Query Match: 61.01% Indels: 10  
 DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x Q96KX8 (1-496)

QY 13 ATGAACACCTGTGGTCTTCCTCTCTGGTGGAGCTCTAGATGGGTCTGTCTCAG 72  
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 73 GTGACGCTACAGAGTGGGGCGCAGGACTGTGAAGCTTCGGAGACCTGTCCCTCACC 132  
 DB 21 LeuGlnLeuGlnSerGlyProGlyLeuValLysSerSerGluThrLeuSerLeuThr 40  
 QY 133 TGGCGTGTCTATCGTGGTCTCTTC-----AGTGGTTACTACGGAGCTGGATCCGCCAG 186  
 DB 41 CysThrValSerGlySerIleSerSerSerSerTyrTrpGlyTrpIleArgGln 60  
 QY 187 CCACAGGTAAGGCTCTGAGTGGATGGTGAATCAATCATAGTGAAGACCAACTAC 246  
 DB 61 ProProGlyLysGlyLeuGluTrpIleAlaAsnThrTyrTyrSerGlyIleThrTyr 80  
 QY 247 AACCGTCTCTAAGAGTGGAGTACCATATAGTAGACACAGTCCAAAGAACCAAGTCTCT 306  
 DB 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnLeuSer 100  
 QY 307 CTGAACACTGAGCTCTGACCGTGGGACACGGCTGTGTATTACTGTGGAGA-----360  
 DB 101 LeuLysValArgSerValThrAlaAlaAspThrAlaValTyrPheCysAlaArgHisGly 120  
 QY 361 -----GTAATTAATTGTTCCGACCTTGGGGCCAGGAAACCTGTGTACC 405  
 DB 121 TyrSerArgSerGlyArgThrGlyAlaIleAspTyrTrpGlyGlnGlyThrLeuValThr 140  
 QY 406 GTCTCTCAGCTCAACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCCAAAGAC 465  
 DB 141 ValSerSerAlaSerProThrSerProLysValPheProLeuSerLeuLysSer---Thr 159  
 QY 466 ACCTCTGGGGGACACGGGCCCTGGGTCTGGTCAAGGACTACTTCCCGAA 519  
 DB 160 GlnProAspGlyAsnValValIleAlaCysLeuValGlnGlyPhePheProGln 177

RESULT 8

O95973  
 ID O95973 PRELIMINARY; PRT; 150 AA.  
 AC O95973;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE VH4 heavy chain variable region precursor (Fragment).  
 GN IGM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Sun C.-H., Song C.-H., Lee C.-H., Lee S.-K.;  
 RA

RT "Clonal proliferation of IgM secreting B cell in the synovium of  
 Behcet's patient with arthritis.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF103795; AAC79084.1; --  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 >150 VH4 HEAVY CHAIN VARIABLE REGION.  
 FT NON\_TER 150  
 SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Alignment Scores:  
 Pred. No.: 8,286-50 Length: 150  
 Score: 583.50 Matches: 115  
 Percent Similarity: 84.21% Conservative: 13  
 Best Local Similarity: 75.66% Mismatches: 19  
 Query Match: 60.34% Indels: 5  
 DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x O95973 (1-150)

QY 13 ATGAACACCTGTGGTCTTCCTCTCTGGTGGAGCTCTAGATGGGTCTGTCTCAG 72  
 DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 73 GTGACGCTACAGAGTGGGGCGCAGGACTGTGAAGCTTCGGAGACCTGTCCCTCACC 132  
 DB 21 LeuGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuSer 40  
 QY 133 TGGCGTGTCTATGGTGGTCTCTTCAGT-----GGTTACTACGGAGCTGGATCCGCCAG 186  
 DB 41 CysThrValSerGlySerIleSerSerSerThrAsnTyrTyrTrpGlyTrpIleArgGln 60  
 QY 187 CCACAGGTAAGGCTGTGGATGGATGGTGAATCAATCATAGTGAAGACCAACTAC 246  
 DB 61 ProProGlyLysGlyLeuGluTrpIleGlySerLeuHisAsnSerGlySerAspTyr 80  
 QY 247 AACCGTCTCTAAGAGTGGAGTCCAGCATATAGTAGACACAGTCCAAAGAACCAAGTCTCT 306  
 DB 81 AsnProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 100  
 QY 307 CTGAACACTGAGCTCTGTGACCGTGGGACACGGCTGTGTATTACTGTGGAGAGTA---363  
 DB 101 LeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgLeuGly 120  
 QY 364 ATTAATTGGTTCGACCTTGGGGCCAGGAAACCTGGTCCAGCTCTCTCAGCTCAACC 423  
 DB 121 MetGlyAlaPheAspPheTrpGlyHisGlyThrMetValThrValSerSerGlySerAla 140  
 QY 424 AAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCTCC 459  
 DB 141 SerAlaProThrLeuPhePro-----ProSerSer 150

RESULT 9

O8TC77  
 ID O8TC77 PRELIMINARY; PRT; 471 AA.  
 AC O8TC77;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 51.8 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Strausberg R.;



RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035041; AAD56277.1; -;  
 DR HSSP; P01825; 7FAB.

DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 FT NON TER 1 119  
 FT NON TER 119 119  
 SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Alignment Scores:  
 Pred. No.: 1,4e-40 Length: 119  
 Score: 491.00 Matches: 95  
 Percent Similarity: 85.71% Conservative: 7  
 Best Local Similarity: 79.83% Mismatches: 13  
 Query Match: 50.78% Indels: 4  
 DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x Q9UL73 (1-119)

QY 70 CAGGTCCACAGCAGTGGGGCGGCGAGCTGTTCAAGCTTCGAGACCTTCCTC 129  
 Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 20  
 QY 130 ACTGCGCTGTCTATGCTGCTCTCTCAGTGGTTACTACTGAGCTGGATCGCCAGCCA 189  
 Db 21 ThrCysThrValSerGlyGlySerIleCysSerTyrTyrTrpSerTrpIleArgGlnPro 40  
 QY 190 CAGGTAAGGCTGCTGAGTGGATGTGTAATCAATCATAGTGGAGACCACTACAAC 249  
 Db 41 ProGlyLysGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrThr 60  
 QY 250 CCGTCTCTCAAGAGTCAGTCCACCATCATAGTAGACACGTCGAGACCACTCTCTG 309  
 Db 61 ProSerLeuLysSerArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeu 80  
 QY 310 AAAGTCAAGCTCTGACCGCTGGGACACGGCTGTATTACTGTCCGAGAGTAATAAT 369  
 Db 81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyrPheCysAlaArgLeuSerAsn 100  
 QY 370 TGG-----TTCACACCTTGGGCGCAGGGAACCTGTCTACCGTCTCTCTCA 414  
 Db 101 TrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 119

RESULT 12

Q9D8L4 PRELIMINARY; PRT; 473 AA.  
 AC Q9D8L4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 1810060009Rik protein.  
 GN IGH-1 OR 1810060009RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCB\_TaxId=10090;  
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fietcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK007918; BAB25349.1; -;  
 DR HSSP; P01842; 7FAB.  
 DR MGD; MGI:96443; Igh-1.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; Ig\_Like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Alignment Scores:  
 Pred. No.: 3,14e-36 Length: 473  
 Score: 449.00 Matches: 87  
 Percent Similarity: 67.82% Conservative: 31  
 Best Local Similarity: 50.00% Mismatches: 52  
 Query Match: 46.43% Indels: 4  
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q9D8L4 (1-473)

QY 13 ATGAACACCTGTGTGTTCTCTCTCTGTGGCAGCTCTAGATGGGTCTGTCTCAG 72  
 Db 1 MetGluTrpSerTrpValPheLeuPheLeuLeuSerValThrAlaGlyValHisCysGln 20  
 QY 73 GTGCGACTACAGCAGTGGGGCGGCGAGGACTGTGAAGCCTTCGAGACCTCTCCCTCACC 132  
 Db 21 ValGlnLeuLysGlnSerGlyAlaGluLeuValLysProGlyAlaSerValLysIleSer 40  
 QY 133 TCGCGCTGTATGTTGTTCTCTCAGTGGTGTACTGAGCTGGATCGCCAGCCACCA 192  
 Db 41 CysLysAlaSerGlyTyrThrPheThrAspTyrTyrIleAsnTrpValLysGlnArgPro 60  
 QY 193 GGTAAGGGTCTGGAGTGGATTGGTGAATCAAT---CATAGTGAAGACCACTACAAC 249  
 Db 61 GlyGlnGlyLeuGluTrpIleGlyLysIleGlyProGlySerGlySerThrTyrTyrAsn 80  
 QY 250 CCGTCTCTCAAGAGTCGAGTCCACCATATCAGTAGACACGTCGAGACCAAGACCTCTCTCT 309  
 Db 81 GluLysPheLysGlyLysAlaThrLeuThrAlaAspLysSerSerSerThrAlaTyrMet 100  
 QY 310 AAAGTCAAGCTCTGTGACCGCTGGGACACGGCTGTATTACTGTCTGGAGAGTA----- 363  
 Db 101 GlnLeuSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgSerGlyTyr 120  
 QY 364 ---ATTAATTGGTTGTCACCCCTTGGGCGCAGGGAACCTGTCTACCCCTCTCTCAGGCTCA 420  
 Db 121 AspTyrAspTrpPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAlaLys 140  
 QY 421 ACCAAGGGCCCATCGGTCTTCCCTTCGACACCTCTCTCCCAAGAGCACCTCTGGGGGCACA 480  
 Db 141 ThrThrAlaProSerValTyrProLeuAlaProValCysGlyGlyThrThrGlySerSer 160  
 QY 481 CGGGCCCTGGGTGCTGTCTGCTCAAGACTACTTCCCGGACCG 522  
 Db 161 ValThrLeuGlyCysLeuValLysGlyTyrPheProGluPro 174



## RESULT 13

Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.  
 AC Q921K1;  
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Unknown (protein for MGC:18977).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012207; AAH12207.1;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 2  
 SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

## Alignment Scores:

Pred. No.: 1,55e-35 Length: 278  
 Score: 441.50 Matches: 88  
 Percent Similarity: 67.26% Conservatives: 25  
 Best Local Similarity: 52.38% Mismatches: 50  
 Query Match: 45.68% Indels: 5  
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q921K1 (1-278)

QY 34 CTCCTCTCTGGGAGCTCCTAGATGGCTCTGTCTAGGTGACGTACAGCATGGGGC 93  
 DB |||||  
 QY 94 GCAGGAGTGTGAAGCTTCGAGACCTCGCTCCCTCGCTGCTCTATGGTGGTTC 153  
 DB |||||  
 QY 28 AlaGluLeuValProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThr 47  
 DB |||||  
 QY 154 TTCAGTGTGTACTAGGAGCTGATCGCCAGCCAGCCAGGTAAAGGTCTGGAGTGGATT 213  
 DB |||||  
 QY 48 PheThrSerTyrTrpMetHisTrpValLysGlnArgGlyGlnGlyLeuGluTrpIle 67  
 DB |||||  
 QY 214 GGTGAATCAAT---CATAGTGAAGACCACTACACCGCTCTCTCAAGATCGAGTC 270  
 DB |||||  
 QY 68 GlyAsnIleAsnProAsnSerGlyGlyThrAsnTyrAsnGlnLysPheLysAsnLysAla 87  
 DB |||||  
 QY 271 ACCATATCAGTACAGCTCCAGAACCAAGTTCCTCTGAACTGAGCTCTGTGACCGCT 330  
 DB |||||  
 QY 88 ThrLeuAlaValAspLysSerSerSerThrValTyrMetGlnLeuSerSerLeuThrSer 107  
 DB |||||  
 QY 331 CGGACACAGCTGTGTATTACTGTGCGAGAGTAAATTAAT-----TGGTTTCGAC 378  
 DB |||||  
 QY 108 GluAspSerAlaValTyrCysThrArgGlyTyrGlyTyrAspValTyrPheAsp 127  
 DB |||||  
 QY 379 CTTTGGGGCAGGAACTTCCTGTCACCGCTCTCTGAGCTCAACCAAGGCCCATCGGTC 438  
 DB |||||  
 QY 128 ValTrpGlyAlaGlyThrValThrValSerSerAlaLysThrThrAlaProSerVal 147  
 DB |||||  
 QY 439 TTCCCTCTGGCACCTCTCAAGAGACCTCTGGGGGCACACGGCCCTGGGCTGCTG 498  
 DB |||||  
 QY 148 TyrProLeuAlaProValCysGlyGlyThrThrGlySerSerValThrLeuGlyCysLeu 167  
 DB |||||  
 QY 499 GTCAAGGACTACTTCCCGCAACCG 522  
 DB |||||  
 QY 168 ValLysGlyTyrPheProGluPro 175  
 DB |||||

## RESULT 14

Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.  
 AC Q99L31;  
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE Similar to RIKEN CDNA I810060009 gene.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003878; AAH03878.1;  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR SMART; SM00410; IG\_like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

## Alignment Scores:

Pred. No.: 1,98e-33 Length: 468  
 Score: 421.00 Matches: 84  
 Percent Similarity: 63.22% Conservatives: 26  
 Best Local Similarity: 48.28% Mismatches: 60  
 Query Match: 43.54% Indels: 4  
 DB: 11 Gaps: 2

US-08-728-463B-219 (1-524) x Q99L31 (1-468)

QY 13 ATGAACACCTGTGTGTTCTCTCTCTGTTGGCAGCTCTAGATGGTCTGTCTCAG 72  
 DB |||||  
 QY 73 GTGACGTACAGCTGGGGCGCAGGACTGTGAAGCTTCGGAGACCTCTCCCTCACC 132  
 DB |||||  
 QY 21 ValGlnLeuGlnGlnSerGlyAlaGluLeuValArgProGlyAlaSerValLysLeuSer 40  
 DB |||||  
 QY 133 TCGCTGTCTATGTGTGTCTCTCTCTGTTTACTTCTGAGCTGATCCGCGCCACCA 192  
 DB |||||  
 QY 41 CysThrAlaSerGlyPheAsnIleLysAspSerLeuMetHisTrpValLysGlnArgPro 60  
 DB |||||  
 QY 193 GGTAGGCTCTGAGTGGATTGGTGAATCAAT---CATAGTGAAGCACCACTACAAC 249  
 DB |||||  
 QY 61 GluGlnGlyLeuGluTrpIleGlyTrpIleAspProGluAspGlyGluThrLysTyrAla 80  
 DB |||||  
 QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTACAGTCCAGACACCAAGACCTCTCTG 309  
 DB |||||  
 QY 81 ProlLysPheGlnAspLysAlaThrIleThrAlaAspThrSerSerAsnThrAlaTyrLeu 100  
 DB |||||  
 QY 310 AAATGAGCTCTGACCGCTGCGACACCGCTGTGTATTACTGTGCGAGAGTAAT--- 366  
 DB |||||  
 QY 101 GlnLeuSerSerLeuThrSerGluAspThrAlaIleTyrTyrCysAlaArgAsnLeuLeu 120  
 DB |||||  
 QY 367 -----AATGGTTCGACCTTCGGGGCAGGAGACCTGTGTCACCGTCTCTCAGCTCA 420  
 DB |||||  
 QY 121 TyrGlyGlyTyrTyrAspTyrTrpGlyGlnGlyThrThrIleThrValSerSerAlaLys 140  
 DB |||||  
 QY 421 ACCAAGGCCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGACCTCTGGGGGCACA 480  
 DB |||||  
 QY 141 ThrThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSer 160  
 DB |||||  
 QY 481 CGGCCCTGGCTGCTGTCAGGACTACTTCCCGAACC 522  
 DB |||||  
 QY 161 ValThrLeuGlyCysLeuValLysGlyTyrPheProGluPro 174  
 DB |||||

RESULT 15



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Q8VDC9	PRELIMINARY;	PRT;	168 AA.
AC	Q8VDC9;		
DT	01-MAR-2002 (TRENBLrel. 20, Created)		
DT	01-MAR-2002 (TRENBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)		
DE	Anti-MOG 212 variable gamma 2a (Fragment).		
GN	IGG2A.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
SEQUENCE	FROM N.A.		
RC	STRAIN=BALB/C;		
RA	Chernajovsky Y.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
SEQUENCE	FROM N.A.		
RC	STRAIN=BALB/C;		
RA	Sembi P.;		
RT	"Targeting T cells to the CNS.";		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ416332; CAC94867.1;		
DR	InterPro; IPR003599; Ig_MHC.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	InterPro; IPR001230; Prenyl_site.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SMC0409; IG; 1.		
DR	SMART; SMC0406; IGv; 1.		
DR	PROSITE; PS00294; PRENYLATION; UNKNOWN_1.		
FT	NON_TER 168 168		
SQ	SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;		

Alignment Scores:			
Pred. No.:	1,93e-33	Length:	168
Score:	420.00	Matches:	84
Percent Similarity:	64.29%	Conservative:	24
Best Local Similarity:	50.00%	Mismatches:	56
Query Match:	43.43%	Indels:	4
DB:	11	Gaps:	2

US-08-728-463B-219 (1-524) x Q8VDC9 (1-168)			
QY	13	ATGAACACCTGTGGTTCTTCCTCTCTGGTGGCAGCTCTAGATGGGTCCTGCTCAG	72
Db	1	MetGluTrpThrTrpValPheLeuPheLeuSerValThrAlaGlyValHisSerGln	20
QY	73	GTGCAGCTACACAGTGGGGCGAGACTGTTGAGCTTCGGAGACCTCGGAGACCTGTCCTCAC	132
Db	21	ValGlnLeuGlnSerGlyAlaGluLeuMetLysProGlyAlaSerValLysIleSer	40
QY	133	TCGCGTGTCTATGGTGGTTCCTTCAGTGGTTACTTACTGGAGCTGGATCCGCCAGCCACCA	192
Db	41	CysLysAlaThrGlyTyThrPheSerSerTyTrpIleAspTrpValLysGlnArgPro	60
QY	193	GCTAGAGCTCGGAGTGAATGGTGAATC---AATCATAGTGAAGCACCACCTACAC	249
Db	61	GlyHisGlyLeuGluTrpIleGlyGluIleLeuProGlySerGlyArgThrAsnTyAsn	80
QY	250	CCGTCCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGCTCCAGAACAGGTCTCTCTG	309
Db	81	GluLysPheLysGlyLysThrPheThrAlaAspThrSerSerAsnThrAlaTyrlle	100
QY	310	AAACTGAGCTCTGTGACCGCTGGCAGCACCGCTGTGTATTACTGTGCGAGAGTAATTAAT	369
Db	101	GlnPheSerSerLeuThrSerGluAspSerAlaValTyTyTyCysAlaAsnTyGlySer	120
QY	370	-----TGGTTCGACCTTGGGGCAGGACCTGGTACCGTCTCTCTCAGCCTCA	420
Db	121	SerArgTrpTyPheAspValTrpGlyAlaGlyThrValThrValSerSerThrLys	140

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 13.893 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-219

Perfect score: 967

Sequence: 1 AAGCTTGCCACATGAACA.....GACTACTTCCCGAACCGGT 524

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool/US08728463/runat 03062003.085613.16797/app query.fasta.1.3690  
-DB=A\_Geneseq\_101002 -QFMT=fastan -SUFFIX=rag -MTNMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463@cgn2.1.353 @runat 03062003.085613.16797 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A\_Geneseq\_101002.\*

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	812	84.0	462	21	AAB26884	Human immunoglobulin
2	784.5	81.1	193	23	ABP43199	Human ovarian anti
3	783	81.0	472	17	AAR93166	Anti-rhesus D reco
4	766.5	79.3	473	22	AAB36206	Human immune syste
5	739	76.4	476	18	AAW01822	Primate anti-hu
6	739	76.4	476	19	AAW63765	Macaque primatized
7	739	76.4	476	23	AAU11646	Protein sequence o
8	729	75.4	470	21	AAU44721	Human immune syste
9	722	74.7	476	18	AAW01818	Primate anti-hu
10	722	74.7	476	19	AAW63761	Macaque primatized
11	714.5	73.9	475	17	AAU11539	Protein sequence o
12	706.5	73.1	537	21	AAU96290	Human IGPAM-2 immu
13	706.5	73.1	537	21	AAU96290	Human IGPAM-2 immu
14	700	72.4	467	18	AAW14927	Human gamma-4PE he
15	700	72.4	467	18	AAW14925	Human gamma-4PE he
16	700	72.4	467	18	AAW14926	Human gamma-4PE he
17	699	72.3	528	15	AAU52952	Human anti-IgE MAb
18	680.5	70.4	139	21	AAU99556	Human LH1238 mono
19	622	64.3	116	16	AAU66324	Human immunoglobul
20	615	63.6	487	22	ABU90607	Human secreted pro
21	615	63.6	487	23	ABG54445	Human albumin fusi
22	609.5	63.0	229	21	ABU30593	Variable and first
23	609.5	63.0	256	23	ABG35335	Thrombopoietin ago
24	608	62.9	155	21	AAU64727	Human 5' EST relat
25	607.5	62.8	832	17	AAW04302	Antibody/beta gluc
26	605	62.6	507	21	AAU96304	Human IGPAM-16 imm
27	603	62.4	470	13	AAU22757	Reshaped CAMPATH-1
28	602.5	62.3	266	23	ABG35336	Thrombopoietin ago
29	600.5	62.1	467	13	ABU22759	Reshaped CD4 antib
30	597.5	61.8	249	23	ABP45310	Human BLYS binding
31	597.5	61.8	467	13	ABP22758	Reshaped CD4 antib
32	593.5	61.4	524	23	AAE21618	Human gene 2 encod
33	592.5	61.3	133	23	ABG35331	Thrombopoietin ago
34	590.5	61.1	139	21	AAU82628	Human PTHrP monocl
35	585.5	60.5	172	21	AAU93173	The heavy chain of
36	580.5	60.0	581	22	AAU81972	Ganglioside GD2 sp
37	578	59.8	123	17	AAU03757	Anti-rhesus D mono
38	576.5	59.6	475	22	AAU63640	Amino acid sequenc
39	576	59.6	205	20	AAU34299	IGM antibody CEM 1
40	574.5	59.4	244	20	AAU21883	Amino acid sequenc
41	572	59.2	241	22	AAU46061	Human TF anti-idio
42	565	58.4	142	14	AAU41285	F105 rearranged va
43	564.5	58.4	139	21	AAU64676	Human 5' EST relat
44	564.5	58.4	273	17	AAU05827	Humanised ID10 ant
45	564.5	58.4	446	17	AAU05829	Humanised ID10 ant

# ALIGNMENTS

RESULT 1  
AAB26884  
ID AAB26884 standard; Protein; 462 AA.  
XX  
AC AAB26884;  
XX  
DT 01-FEB-2001 (first entry)  
XX  
DE Human immunoglobulin heavy chain amino acid sequence.  
KW Monoclonal antibody; immunoglobulin heavy chain; human.  
XX Homo sapiens.  
OS  
XX WO200058499-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 30-MAR-2000; 2000WO-JP02022.







PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -  
 XX useful for treating autoimmune disease or graft-versus-host disease  
 PS Claim 14; Fig 10B; 81pp; English.  
 XX  
 CC 2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised  
 CC forms of the light and heavy chains of cynomolgus monkey anti-human  
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and  
 CC heavy variable genes (see also AAT62512 and AAT62513) are inserted into  
 CC an expression vector (pref. NEOSPLA) which contains human light and  
 CC heavy chain constant genes to allow prodn. of the primatised  
 CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1  
 CC antibodies have also been produced (see also AAW01817-20). The  
 CC primatised antibodies inhibit the B7:CD28 pathway, making them  
 CC useful immunosuppressants for the treatment of autoimmune disorders  
 CC and graft-versus-host disease.  
 XX  
 SQ Sequence 476 AA;  
 Alignment Scores:  
 Pred. No.: 7,85e-59 Length: 476  
 Score: 739.00 Matches: 147  
 Percent Similarity: 85.16% Conservative: 8  
 Best Local Similarity: 80.77% Mismatches: 15  
 Query Match: 76.42% Indels: 12  
 DB: 18 Gaps: 4  
 US-08-728-463B-219 (1-524) x AAW01822 (1-476)  
 QY 13 ATGAACACCTGTGGTTCCTCCCTGTCGAGCTCCTAGATGGTCTGTCTCAG 72  
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 73 GTCAGCTACAGCAGTGGGCGCAGGACTGTTGAAGCCTTCGAGACCTGTCCCTCACC 132  
 Db 21 ValGlnLeuGlnSerGlyProGlyLeuValValProSerGlnThrLeuSerLeuThr 40  
 QY 133 TGGCTGTCTATGGTGGTCTCTTCAGT---GGTTACTTGGAGCTGGATCCGCCAGCCA 189  
 Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyArgTrpGlyTrpIleArgGlnPro 60  
 QY 190 CCAAGTAAGGCTCTGAGTGGATTGGTGAATC---AATCATAGTGAAGCACTACTAC 246  
 Db 61 ProGlyLysGlyLeuGlnTrpIleGlySerPheTySerSerGlyAsnThrTyTyr 80  
 QY 247 AACCCGTCTCTCAAGAGTCTGAGTCCACATATCATAGTAGACACGTCACAGAACCACTCTCT 306  
 Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100  
 QY 307 CTGAAGTACGCTCTGTGACCGCTGGGACACGGCTGTGTATTACTGTGGGAGA----- 360  
 Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyTyrCysValArgAspArg 120  
 QY 361 -----GTAATT-----AATTGGTTCGACCTTGGGCGCAGGAACC 396  
 Db 121 LeuPheSerValValGlyMetValTyTrpAsnAsnTrpPheAspValTrpGlyProGlyVal 140  
 QY 397 CTGGTCAACCTCTCTCAGCTCAACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCC 456  
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160  
 QY 457 TCAAGAGCACTCTGGGGGACACGCGGCCCTGGGTCTGTGTCAAGGACTACTTCCCC 516  
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPhePro 180  
 QY 517 GAACCG 522  
 Db 181 GluPro 182  
 RESULT 6  
 AAW63765  
 ID AAW63765 standard; Protein; 476 AA.  
 XX

AC AAW63765;  
 XX 29-SEP-1998 (first entry)  
 DT  
 XX  
 DE Macaque primatised 16C10 heavy chain protein.  
 XX  
 KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;  
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
 KW immunogen; anti-idiotypic reagent; interleukin-2; IGF; immunoglobulin G;  
 KW T cell proliferation.  
 XX  
 OS Macaca fascicularis.  
 XX  
 PN WO9819706-A1.  
 XX  
 PD 14-MAY-1998.  
 XX  
 XX 29-OCT-1997; 97WO-US19906.  
 XX  
 XX 08-NOV-1996; 96US-0746361.  
 XX (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Brans P, Hanna N;  
 XX  
 XX WPI; 1998-286601/25.  
 XX N-P8DB; AAV35489.  
 XX  
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
 PT inhibiting binding to CD28 - useful as specific immunosuppressants  
 PT for treating diseases that involve interactions between T and B  
 PT cells, e.g. graft rejection or tumours  
 XX  
 XX Example 7; Fig 5b; 87pp; English.  
 PS  
 CC This sequence represents a primatised form of the antibody 16C10 heavy  
 CC chain from macaque. This sequence is used in a method which studies new  
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to  
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such  
 CC Mab's are specific immunosuppressants for treatment of diseases involving  
 CC T cell/B cell interactions, particularly autoimmune disease, specifically  
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type  
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,  
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.  
 CC host diseases, B cell lymphoma, infections (including by human immune  
 CC deficiency virus) or inflammatory disease and tumours. Optionally the  
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can  
 CC also be used as imaging agents and as vaccines or immunogens to develop  
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins  
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions  
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits  
 CC production of interleukin-2 (IL-2), T cell proliferation and  
 CC antigen-specific immunoglobulin G (IgG) responses.  
 XX  
 SQ Sequence 476 AA;  
 Alignment Scores:  
 Pred. No.: 7,85e-59 Length: 476  
 Score: 739.00 Matches: 147  
 Percent Similarity: 85.16% Conservative: 8  
 Best Local Similarity: 80.77% Mismatches: 15  
 Query Match: 76.42% Indels: 12  
 DB: 19 Gaps: 4  
 US-08-728-463B-219 (1-524) x AAW63765 (1-476)  
 QY 13 ATGAACACCTGTGGTTCCTCCCTGTCGAGCTCCTAGATGGTCTGTCTCAG 72  
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 73 GTCAGCTACAGCAGTGGGCGCAGGACTGTTGAAGCCTTCGAGACCTGTCCCTCACC 132  
 Db 21 ValGlnLeuGlnSerGlyProGlyLeuValValProSerGlnThrLeuSerLeuThr 40  
 QY 133 TGGCTGTCTATGGTGGTCTCTTCAGT---GGTTACTTGGAGCTGGATCCGCCAGCCA 189  
 Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyArgTrpGlyTrpIleArgGlnPro 60  
 QY 190 CCAAGTAAGGCTCTGAGTGGATTGGTGAATC---AATCATAGTGAAGCACTACTAC 246  
 Db 61 ProGlyLysGlyLeuGlnTrpIleGlySerPheTySerSerGlyAsnThrTyTyr 80  
 QY 247 AACCCGTCTCTCAAGAGTCTGAGTCCACATATCATAGTAGACACGTCACAGAACCACTCTCT 306  
 Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100  
 QY 307 CTGAAGTACGCTCTGTGACCGCTGGGACACGGCTGTGTATTACTGTGGGAGA----- 360  
 Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyTyrCysValArgAspArg 120  
 QY 361 -----GTAATT-----AATTGGTTCGACCTTGGGCGCAGGAACC 396  
 Db 121 LeuPheSerValValGlyMetValTyTrpAsnAsnTrpPheAspValTrpGlyProGlyVal 140  
 QY 397 CTGGTCAACCTCTCTCAGCTCAACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCC 456  
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160  
 QY 457 TCAAGAGCACTCTGGGGGACACGCGGCCCTGGGTCTGTGTCAAGGACTACTTCCCC 516  
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyPhePro 180  
 QY 517 GAACCG 522  
 Db 181 GluPro 182  
 RESULT 6  
 AAW63765  
 ID AAW63765 standard; Protein; 476 AA.  
 XX

Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
 QY 133 TCGCTGTCTATGGTGTCTTCACTGAGTGGAGTGGATCGCCAGCA 189  
 Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyrGlyTyrGlyTyrGlyGlnPro 60  
 QY 190 CCAGGTAAGGCTCTGAGTGGATTGGTGAATC---AATCATAGTGAAGCACCACCACTAC 246  
 Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80  
 QY 247 AACCCGTCTCTCAAGAGTGGATCACCATATCAGTACAGTCCCAAGAACCACTTCTCT 306  
 Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100  
 QY 307 CTGAAGTGTCTGTGACCGCTCGGACAGCGCTGTGTATTACTGTGCGAGA----- 360  
 Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrCysValArgAspArg 120  
 QY 361 -----GTAAAT-----AATTGGTTCGACCTTGGGGCCAGGAAAC 396  
 Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140  
 QY 397 CTGGTCAACCGTCTCTCAGCTCAACCAAGGCGCCATCGGCTTCCCTCGGACCCCTCC 456  
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160  
 QY 457 TCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGACTACTTCCCC 516  
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180  
 QY 517 GAACCG 522  
 Db 181 GluPro 182

## RESULT 7

AAU11646  
 ID AAU11646 standard; Protein; 476 AA.

AC AAU11646;

DT 12-MAR-2002 (first entry)

Protein sequence of primatised form of the heavy chain of 16C10 antibody.

Human; macaque monkey; light chain; primatised antibody; 16C10 antibody;  
 neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
 B7\_1 antigen; CD80; B7\_2 antigen; CD86; B cell cancer; metastasis;  
 tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
 graft-vs-host disease; immunosuppression; organ rejection;  
 interleukin-2; IL-2; mutant; mutein.

OS Chimeric - Homo sapiens.

OS Chimeric - Macaca sp.

OS Synthetic.

OS WO200189567-A1.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Brans P;

XX WPI; 2002-089895/12.

DR N-PSDB; AAS17247.

Use of monoclonal antibody which specifically binds to B7.1 antigen  
 CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,  
 treating cancer, graft-vs-host disease and autoimmune disease such as

PT allergy -

XX Example 8; Fig 5b; 89pp; English.

CC The present invention relates to a new use of a monoclonal antibody  
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is  
 CC useful for treating diseases such as B cell cancer, lymphoma, a  
 CC cancer where B cells promote the growth and/or metastasis of tumours,  
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematous,  
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis  
 CC or graft-vs-host disease. The antibody is useful for immunosuppression  
 CC in a human or animal and for treating or preventing resistance to or  
 CC rejection of transplanted organ or tissue for treating proliferative  
 CC and hyperproliferative diseases, for treating reversible obstructive  
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's  
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,  
 CC rhinitis and eczema, and other types of allergies. The present protein  
 CC sequence represents the heavy chain of 16C10, a primatised antibody  
 CC used in the invention to induce apoptosis and inhibit production of  
 CC interleukin-2 (IL-2).

XX SQ Sequence 476 AA;

## Alignment Scores:

Pred. No.: 7,85e-59 Length: 476  
 Score: 739.00 Matches: 147  
 Percent Similarity: 85.16% Conservative: 8  
 Best Local Similarity: 80.77% Mismatches: 15  
 Query Match: 76.42% Indels: 12  
 DB: 23 Gaps: 4

US-08-728-463B-219 (1-524) x AAU11646 (1-476)

QY 13 ATGAACACCTGTGTGTTCTTCTCTCTGTGGCAGCTCTAGATGGTCTGTCTCAG 72

Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTGCAGCTACAGCAGTGGGGCGCAGGAGCTGTTGAAGCCTTCGGAGACCTGTCTCCAC 132

Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

QY 133 TCGCTGTCTATGGTGTCTTCTTCACTGAGTGGAGTGGATCGCCAGCA 189

Db 41 CysAlaValSerGlyGlySerIleSerGlyGlyTyrGlyTyrGlyTyrGlyGlnPro 60

QY 190 CCAGGTAAGGCTCTGAGTGGATTGGTGAATC---AATCATAGTGAAGCACCACCACTAC 246

Db 61 ProGlyLysGlyLeuGluTrpIleGlySerPheTyrSerSerGlyAsnThrTyrTyr 80

QY 247 AACCCGTCTCTCAAGAGTGGATCACCATATCAGTACAGTCCCAAGAACCACTTCTCT 306

Db 81 AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100

QY 307 CTGAAGTGTCTGTGACCGCTCGGACAGCGCTGTGTATTACTGTGCGAGA----- 360

Db 101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrCysValArgAspArg 120

QY 361 -----GTAAAT-----AATTGGTTCGACCTTGGGGCCAGGAAAC 396

Db 121 LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrpGlyProGlyVal 140

QY 397 CTGGTCAACCGTCTCTCAGCTCAACCAAGGCGCCATCGGCTTCCCTCGGACCCCTCC 456

Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160

QY 457 TCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGACTACTTCCCC 516

Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180

QY 517 GAACCG 522



QY 475 GGCACAGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCGAACCG 522  
 Db 161 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176

## RESULT 9

AAW01818  
 ID AAW01818 standard; Protein; 476 AA.

AC AAW01818;  
 XX 25-MAY-1997 (first entry)

XX Primatised anti-human B7.1 antigen antibody 7C10 heavy chain.

XX Monoclonal antibody; cynomolgus monkey; macaque; 7C10;  
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;  
 KW autoimmune disease; idiopathic thrombocytopenia purpura;  
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes mellitus; graft versus host disease;  
 KW hetero-hybridoma; transfectoma.

XX Chimeric Macaca cynomolgus;  
 OS Chimeric Homo sapiens.

XX WO9640878-A1.

PN 19-DEC-1996.

PD 06-JUN-1996; 96WO-US10053.

PF 07-JUN-1995; 95US-0487550.

PR (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N, Shestowsky WS;

XX WPI; 1997-108638/10.

DR N-PSDB; AAT62510.

XX Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -

PT useful for treating autoimmune disease or graft-versus-host disease

PS Claim 6; Fig 8B; 81pp; English.

XX 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised  
 CC forms of the light and heavy chains of cynomolgus monkey anti-human  
 CC B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy  
 CC variable genes (see also AAT62509 and AAT62510) are inserted into  
 CC an expression vector (pref. NEO9PLA) which contains human light and  
 CC heavy chain constant region genes to allow prodn. of the primatised  
 CC antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1  
 CC antibodies have also been produced (see also AAW01819-22). The  
 CC primatised antibodies inhibit the B7:CD28 pathway, making them  
 CC useful immunosuppressants for the treatment of autoimmune disorders  
 CC and graft-versus-host disease.

XX Sequence 476 AA;

## Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	18	Gaps:	3

US-08-728-463B-219 (1-524) x AAW01818 (1-476)

QY '13 ATGAACACCTGGTGTCTTCCTCCTCGTGGCAGCTCTAGATGGTCTGTCTCAG 72  
 Db 1 MetLysHisLeuTrpPhePheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTGACGTACACGAGTGGGGCCAGCAGCTGTGAAGCCTTCGGAGACCCCTGTCCTCACC 132  
 Db 21 ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGluTrpLeuSerArgThr 40  
 QY 133 TCGCGTCTCTATGGTGGTTCCTTCAGTGT---TACTACTGAGCTGGATCGCCAGCCA 189  
 Db 41 CysValValSerGlyGlySerIleSerGlyTyrTyrTrpTrpTrpIleArgGlnThr 60  
 QY 190 CCAGGTAAAGGTCTCGAGTGGATTGGTGAATCAATCATAGTGA---AGCACCAACTAC 246  
 Db 61 ProGlyArgGlyLeuGluTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr 80  
 QY 247 AACCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCACAGAACCAAGTCTCT 306  
 Db 81 AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe 100  
 QY 307 CTGAAACTGAGCTCTGTGACCTCGGACACGGCTGTATTACTGTGCGAGA----- 360  
 Db 101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrTyrCysAlaArgGlyPro 120  
 QY 361 -----GTAATTAATGTTCGACCTTGGCCCTTGGGGCCAGGGAACC 396  
 Db 121 ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140  
 QY 397 CTGGTCACCGTCTCTCAGCCTCAACCAAGGGCCCATCGTCTTCCCTCGGCACCTCC 456  
 Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160  
 QY 457 TCCAGAGCACCTCTGGGGGCACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCC 516  
 Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180  
 QY 517 GAACCG 522  
 Db 181 GluPro 182

RESULT 10  
 AAW63761  
 ID AAW63761 standard; Protein; 476 AA.  
 XX  
 AC AAW63761;  
 XX 29-SEP-1998 (first entry)  
 DT  
 XX Macaque primatized 7C10 heavy chain DNA.  
 DE  
 XX Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;  
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
 KW immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;  
 KW T cell proliferation; ss.  
 XX Macaca fascicularis.  
 OS  
 XX WO9819706-A1.  
 PN 14-MAY-1998.  
 PD 29-OCT-1997; 97WO-US19906.  
 PF 08-NOV-1996; 96US-0746361.  
 PR (IDEC-) IDEC PHARM CORP.  
 PA Anderson DR, Brams P, Hanna N;  
 PI WPI; 1998-286601/25.  
 XX DR N-PSDB; AAV35485.  
 DR  
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and  
 PT inhibiting binding to CD28 - useful as specific immunosuppressants  
 PT for treating diseases that involve interactions between T and B  
 PT cells, e.g. graft rejection or tumours

```

Db      181 GIUPro 182
RESULT 8
AAY44721
ID      AAY44721 standard; Protein; 470 AA.
XX
AC      AAY44721;
XX
DT      25-APR-2000 (first entry)
XX
DE      Human immune system molecule, ISMO-2.
XX
KW      Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
KW      treatment; prevention; cell proliferation; immune system disorder.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Peptide
FT      1..19
FT      /label= Signal_peptide
FT      Protein
FT      20..470
FT      /label= Mature_ISMO-2
FT      Modified-site
FT      120
FT      /note= "N-glycosylated"
FT      Modified-site
FT      320
FT      /note= "N-glycosylated"
FT      Modified-site
FT      105
FT      /note= "Casein kinase II phosphorylation site"
FT      Modified-site
FT      232
FT      /note= "Casein kinase II phosphorylation site"
FT      Modified-site
FT      290
FT      /note= "Casein kinase II phosphorylation site"
FT      Modified-site
FT      377
FT      /note= "Casein kinase II phosphorylation site"
FT      Modified-site
FT      47
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      81
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      92
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      98
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      142
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      154
FT      /note= "Protein kinase C phosphorylation site"
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FT      /note= "Protein kinase C phosphorylation site"
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FT      /note= "Protein kinase C phosphorylation site"
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FT      460
FT      /note= "Protein kinase C phosphorylation site"
FT      Modified-site
FT      69
FT      /note= "Tyrosine kinase phosphorylation site"
FT      Modified-site
FT      319
FT      /note= "Tyrosine kinase phosphorylation site"
FT      Region
FT      387..409
FT      /note= "conserved Ig/MHC protein block"
FT      Region
FT      446..463
FT      /note= "conserved Ig/MHC protein block"
FT      Domain
FT      34..116
FT      /note= "shows similarity to Ig superfamily protein
FT      domain"
FT      160..225
FT      /note= "shows similarity to Ig superfamily protein
FT      domain"
FT      383..450
FT      /note= "shows similarity to Ig superfamily protein
FT      domain"
WO200000608-A2.

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PD      06-JAN-2000.
XX
XX      21-JUN-1999; 99WO-US13995.
XX
PR      30-JUN-1998; 98US-0107223.
XX
PA      (INCY-) INCYTE PHARM INC.
XX
PI      Lal P, Tang YT, Corley NC, Gorgone G, Guegler KJ, Patterson C;
PI      Baughn MR;
XX
XX      WPI; 2000-170916/15.
DR      N-PSDB; AAZ50012.
XX
PT      Immune system molecules used in the diagnosis, treatment and prevention
PT      of disorders associated with the immune system and cell proliferation
PT
XX
XX      Claim 1; Pages 60-61; 69pp; English.
XX
CC      The present sequence is an immune system molecule,
CC      ISMO-2 from an Incyte clone 2849752 isolated from the human breast
CC      tumour cDNA library (BRSTUT13). This sequence is expressed in several
CC      libraries, generally those associated with cancer, cell
CC      proliferation, immune response or trauma. It shows homology to
CC      vertebrate immunoglobulin gamma heavy-chain.
CC      The present sequence is useful in the diagnosis, treatment and
CC      prevention of disorders associated with the immune system and
CC      cell proliferation.
XX
SQ      Sequence 470 AA;
Alignment Scores:
Pred. No.: 6,348-58 Length: 470
Score: 729.00 Matches: 144
Percent Similarity: 85.23% Conservative: 6
Best Local Similarity: 81.82% Mismatches: 20
Query Match: 75.39% Indels: 6
DB: 21 Gaps: 1
US-08-728-463B-219 (1-524) x AAY44721 (1-470)
QY      13 ATGAACACCTGTGTTCTTCTCTCTCTGTGTCAGCTCTAGATGGTCTCTCTCAG 72
Db      1 MetlyshisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY      73 GTGAGCTACAGCAGTGGCGGCGAGGACTGTGAAGCTTCGAGACCCCTGCTCACC 132
Db      21 ValGlnLeuGlnGluSerGlyProGlyLeuVallyserProSerGluThrLeuSerLeuThr 40
QY      133 TGCCTGTCTATGTTGTTCTCTCTCAGTGTCTACTCTGAGCTGGATCCGCCAGCCACCA 192
Db      41 CysThrValSerGlyGlySerIleArgSerTyrTrpAsnTrpIleArgLeuProPro 60
QY      193 GGTAAAGGCTCGAGTGGATGTGTAATCAATCATAGTCGAAGCACCACCACTACACCCG 252
Db      61 GlyLygLyLeuGluTrpIleGlyTyrIleTyrThrSerGlySerThrAsnTyrAsnPro 80
QY      253 TCTCTAAGAGTCGAGTCACCATATCAGTACAGCAGCTCCAGAACACAGTTCTCTGAAA 312
Db      81 SerLeuLysserArgValThrMetSerValAspThrSerLysserLysserGlnPheSerLeuLys 100
QY      313 CTGAGCTCTGTGACCGCTGCGGACACGGCTGTGTATTACTTGTCCGAGA----- 360
Db      101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgProProAsn 120
QY      361 -----GTAATTAAATTGGTTCGACCTTGGGGCCAGGAAACCTGTGCTACCGTCTCTCA 414
Db      121 AlaThrThrThrThrValTrpThrSerGlyAlaLysGlyAlaLeuValThrValSerSer 140
QY      415 GCCTCAACCAAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCCAAAGACGACCTCTGGG 474
Db      141 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysserThrSerGly 160

```

XX

PS Example 7; Fig 3b; 87pp; English.

XX This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotypic reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.

XX Sequence 476 AA;

## Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	19	Gaps:	3

US-08-728-463B-219 (1-524) x AAW63761 (1-476)

QY	13	ATGAACACCTGGTGGTCTTCCTCCCTGGTGGCAGCTCCTAGATGGTCTGTCTCAG	72
DB	1	MetLysHisLeuTrpPheLeuLeuLeuValAlaAlaProArgTrpValLeuSerGln	20
QY	73	GTGACGCTACAGCAGTGGGGCGCAGGACTGTTGAACCTTCGGAGACCTGTCCCTCACC	132
DB	21	ValLysLeuGlnGlnTrpGlyGluGlyLeuLeuGlnProSerGlnThrLeuSerArgThr	40
QY	133	TGCGCTGTCTATGTTGGTTCCTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA	189
DB	41	CysValValSerGlyGlySerIleSerGlyTyrTyrTrpTrpTrpIleArgGlnThr	60
QY	190	CCAGGTAAGGGCTGGAGTGGATTGGTGAATCAATCATAGTGG---AGCACCAACTAC	246
DB	61	ProGlyArgGlyLeuGlnTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr	80
QY	247	AACCCGTCTCTCAAGAGTCGAGTCACCATATCATAGTACACAGTCACCAAGAACCATGTTCTCT	306
DB	81	AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe	100
QY	307	CTGAACACTGAGCTCTGACCGCTGGGACACGGCTGTGTATTACTGTGGAGA-----	360
DB	101	LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrCysAlaArgGlyPro	120
QY	361	-----GTAATTAAATGGTTCGACCTTCGACCTGGGCCAGGGAACC	396
DB	121	ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp	140
QY	397	CTGGTCACCGCTCTCCCTCAGCCTCAACCAAGGGGCCCATCGCTCTTCCCTGGCACCTCC	456
DB	141	LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer	160
QY	457	TCAAGAGCACCTCTCGGGGCGACAGCGGCCCTGGCTGGCTGGCTCAAGCACTACTTCCC	516
DB	161	SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro	180
QY	517	GAACCG	522
DB	181	GluPro	182

## RESULT 11

AAU11539 standard; Protein; 476 AA.

XX AAU11539;

DT 12-MAR-2002 (first entry)

DE Protein sequence of primatized form of the heavy chain of 7C10 antibody.

KW Human; macaque monkey; light chain; primatized antibody; 7C10 antibody;  
 KW neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;  
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;  
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;  
 KW graft-vs-host disease; immunosuppression; organ rejection;  
 KW interleukin-2; IL-2; mutant; mutein.

XX Chimeric - Homo sapiens.

OS Chimeric - Macaca sp.

OS Synthetic.

XX WO200189567-A1.

XX 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US16364.

XX 22-MAY-2000; 2000US-0576424.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Brams P;

XX WPI: 2002-089895/12.

XX N-PSDB; AAS17243.

PT Use of monoclonal antibody which specifically binds to B7.1 antigen  
 CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,  
 PT treating cancer, graft-vs-host disease and autoimmune disease such as  
 PT allergy

XX Example 8; Fig 3b; 89pp; English.

XX The present invention relates to a new use of a monoclonal antibody  
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen  
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is  
 CC useful for treating diseases such as B cell cancer, lymphoma, a  
 CC cancer where B cells promote the growth and/or metastasis of tumours,  
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as  
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,  
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic  
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis  
 CC or graft-vs-host disease. The antibody is useful for immunosuppression  
 CC in a human or animal and for treating or preventing resistance to or  
 CC rejection of transplanted organ or tissue for treating proliferative  
 CC and hyperproliferative diseases, for treating reversible obstructive  
 CC airways disease, intestinal inflammations and allergies e.g. Crohn's  
 CC disease and ulcerative colitis, food-related allergies e.g. migraine,  
 CC rhinitis and eczema, and other types of allergies. The present protein  
 CC sequence represents the heavy chain of 7C10, a primatized antibody  
 CC used in the invention to induce apoptosis and inhibit production of  
 CC interleukin-2 (IL-2).

XX Sequence 476 AA;

## Alignment Scores:

Pred. No.:	2,75e-57	Length:	476
Score:	722.00	Matches:	143
Percent Similarity:	82.42%	Conservative:	7
Best Local Similarity:	78.57%	Mismatches:	20
Query Match:	74.66%	Indels:	12
DB:	23	Gaps:	3

ID AAY96290 standard; protein; 537 AA.





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QY	13	ATGAACACCTGTGTTCTTCTCTCTGTGTGCAGCTCTAGATGGGCTGTGTCTCAG	72
Db	1	MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln	20
QY	73	GTGCAGCTACACGACTGGGGCGGAGGACTGTTGAAGCTTCGGAGACCTGTCCTCAC	132
Db	21	ValGlnLeuGlnLuserGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr	40
QY	133	TCCGCTGTCTATGGTGGTTCTCTCAGTGGT---TACTACTGGAGCTGGATCGCCACGCA	189
Db	41	CysSerValSerGlyGlySerIleSerGlyAspTrpTrpPheTrpIleArgGlnSer	60
QY	190	CCAGGTAAGGGTCTGGAGTGGATGGTGGTAATCAATCATAGT---GGAAGCACCACTAC	246
Db	61	ProGlyLysGlyLeuGluTrpIleGlyTyrlleTyrglySerGlyGlyThrAsnTrp	80
QY	247	RACCGCTCTTCAGAGTCCGAGTCCACCATTCAGTAGACGACGTCCCAAGAACAGTTCTCT	306
Db	81	AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer	100
QY	307	CTGAAACTGAGCTCTGTGACCGCTGGCGACACGGCTGTGTATTACTGTCGG-----	357
Db	101	LeuLysLeuAsnGlySerValThrAlaAlaAspThrAlaValTyrcysAlaSerAsnIle	120
QY	358	---AGAGTAATTATTGGTTCGACCCCTGGGGCGGGAACCGTGGTCACTCTCTCTCA	414
Db	121	LeuLysTyrlLeuHisTrpLeuLeuTyrrTrpGlyGlnGlyValLeuValThrValSerSer	140
QY	415	GCCTCAACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCCAAGAGCACCTTCGG	474
Db	141	AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu	160
QY	475	GGCACAGGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG	522
Db	161	SerThrAlaAlaLeuGlyCysLeuValLysAspTyrrPheProGluPro	176

Search completed: June 3, 2003, 09:02:28  
Job time : 39.0597 secs









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1 APPLICANT: Hanna, Nabil
2 Newman, Roland A.
3 Reff, Mitchell E.
4 TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
5 Therapy
6 NUMBER OF SEQUENCES: 59
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
9 STREET: 699 Prince Street
10 CITY: Alexandria
11 STATE: VA
12 COUNTRY: USA
13 ZIP: 22314-3187
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent in Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/10/211,357
21 FILING DATE: 05-Aug-2002
22 CLASSIFICATION: <Unknown>
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US/09/612,914A
25 FILING DATE: 10-Jul-2000
26 APPLICATION NUMBER: US 08/523,894
27 FILING DATE: 06-SEP-1995
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Teskin, Robin L.
30 REGISTRATION NUMBER: 35,030
31 REFERENCE/DOCKET NUMBER: 012712-165
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 703-836-6620
34 TELEFAX: 703-836-2021
35 INFORMATION FOR SEQ ID NO: 8:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 467 amino acids
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
41 US-10-211-357-8
42
43 Alignment Scores:
44 Pred. No.: 1.31e-51 Length: 467
45 Score: 700.00 Matches: 139
46 Percent Similarity: 84.66% Conservative: 10
47 Best Local Similarity: 78.98% Mismatches: 21
48 Query Match: 72.39% Indels: 6
49 DB: 9 Gaps: 3
50
51 US-08-728-463B-219 (1-524) x US-10-211-357-8 (1-467)
52
53 QY 13 ATGAACACCTGTGTTCTTCCTCCCTCGTGGGAGCTCTAGATGGTCCCTGCTCT
54 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaIapAOAgtTrpValLeuSerLeu
55
56 QY 73 GTGCAGCTACAGCAGTGGGGCCGACGAGCTGTGTAAGCCCTTCGGAGACCCCTGTCTCCCT
57 Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu
58
59 QY 133 TGCCTCTCTATGGTGGTTCCTTCAGTGGT---TACTACTCGAGCTGGATCCGCCGAC
60 Db 41 CysSerValSerGlyGlySerLeuGlyAspTyrTrpPheTrpLeuAArgGln
61
62 QY 190 CCAGTAAGGGTCTGGAGTGGATTGGTGAATCAATCATAGT---GGAAGCACCAACAA
63 Db 61 ProGlyLysGlyLeuGlnTrpIleGlyTyrIleTyrGlySerGlyGlyThr
64
65 QY 247 AACCGTCTCTCAAGAGTCGAGTCACCATATACAGTAGACAGTCCAAAGAACCAAGTTC
66 Db 81 AsnProSerLeuAsnArgValSerLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeu

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.: 6,56e-43 Length: 249
Score: 597.50 Matches: 121
Percent Similarity: 71.75% Conservative: 6
Best Local Similarity: 68.36% Mismatches: 16
Query Match: 61.79% Indels: 34
DB: 9 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-880-748-1321 (1-249)
QY 70 CAGGTGAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCTTCGGAGACCTGTGCTCC 129
Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20
QY 130 ACCTGCGCTGTATGTTGTTCTTCAGTGGTTACTGAGCTGGATCCGCCAGCCA 189
Db 21 ThrCysAlaValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40
QY 190 CCAGTTAAGGCTGGAGTGGTGAATCAATCATAGTGAAGCACCACCACTACAAC 249
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAenHisSerGlySerThrAsnTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCCAGTCCACATATCAGTAGACACGTCACCAAGAACCACTCTCTG 309
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 310 AAAGTACGCTGTGACCGCTGGGACACCGCTGTGTATTACTGTGCGAGA----- 360
Db 81 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgGlyProArg 100
QY 361 -----GTAAATTAATGTTTCACCTTGGGCGCCAGGAAGC 396
Db 101 TyrTyrAspIleLeuThrGlyTyrArgTyrAsnTrpPheAspProTrpGlyArgGlyThr 120
QY 397 CTGCTCACCTCTCTCCAGCCTCA----- 420
Db 121 LeuValThrValSerSerGlyGlyGlyGlyGlySerGlyGlyGlyGlyGly 140
QY 421 -----ACCAAGGGCCCATCGGTCTTCCCTCCGACACCTCTCCCAAGAGC 465
Db 141 SerAspIleValMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgVal 160
QY 466 ACC-----TCTGGGGCACAGCGCCCTGGCTGGCTGG 499
Db 161 ThrIleThrCysArgAlaSerGlnGlyIleSerSer-TripLeuAlaTrp 176

RESULT 12
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; Sequence 21, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/233042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-21

Alignment Scores:
Pred. No.: 6,71e-42 Length: 172
Score: 585.50 Matches: 118
Percent Similarity: 82.19% Conservative: 2

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1321

Alignment Scores:
Pred. No.: 1.14e-40 Length: 152
Score: 571.00 Matches: 118
Percent Similarity: 82.19% Conservative: 2
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Query Match: 60.55% Indels: 5
DB: 9 Gaps: 2

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QY 91 GCGCAGGAGCTGTTGAAGCTTCGGAGACCTGTGCTCCCTCACCTGGCTGTCTATGTTG 150
Db 2 GlyProGlyLeuValLysProSerGlnIleLeuSerLeuThrCysThrValSerGlyGly 21
QY 151 TCCTTCAGT---T---GGTTACTACTGGAGCTGGATCCGCCAGCACCACAGGTAAAGGTCTG 204
Db 22 SerIleSerSerGlyGlyHisTyrTrpSerTrpIleArgGlnHisProGlyLysGlyLeu 41
QY 205 GAGTGGATTGGTAATCAATCATAGTGAAGCACCACCACTACAACCCGCTCTCAAGAGT 264
Db 42 GluTrpIleGlyTyrIleTyrTrpIleGlyAsnThrTyrAsnProSerLeuLysSerVal 61
QY 265 CGAGTCACCATATCAGTAGACACGTCACCAAGAACCACTGTCTCTGAAACTGAGCTCTGTG 324
Db 62 ArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLysLeuSerVal 81
QY 325 ACCGTGCGGACACCGCTGTGTATTACTGTGCGAGAGTAATTAATGTTTC----- 375
Db 82 ThrAlaAlaAspThrAlaValTyrCysAlaArgAspSerGlyAspTyrTyrGlyIle 101
QY 376 GACCTTGGGGCGCAGGACCTGCTCACCGTCTCTCAGCTCTCAACCAAGGCCCATCG 435
Db 102 AspValTrpGlyGlnGlyThrThrValThrValSerSerAlaSerThrLysGlyProSer 121
QY 436 GTCTTCCCTCCGACCTCTCTCCAGAGACACCTCTGGGGGCACAGCGCCCTGGGCTGC 495
Db 122 ValPheProLeuAlaProCysSerArgSerThrSerGluSerThrAlaAlaLeuGlyCys 141
QY 496 CTGGTCAAGGACTACTTCCCGAAGCCG 522
Db 142 LeuValLysAspTyrPheProGluPro 150

RESULT 13
US-09-187-693-68
; Sequence 68, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Growth Factor Receptor
; CURRENT APPLICATION NUMBER: US/09/187,693
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 152
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(152)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-68

Alignment Scores:
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Score: 571.00 Matches: 118
Percent Similarity: 82.19% Conservative: 2
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Percent Similarity: 74.07%    Conservative: 7  
Best Local Similarity: 69.75%    Mismatches: 22  
Query Match: 57.81%    Indels: 20  
DB: 9    Gaps: 2

US-08-728-463B-219 (1-524) x US-09-880-748-957 (1-249)

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QY	130	ACCTGGCTGTCTATGGTGTCTTCCTTCACTGTTACTACTGGAGCTGGATCCGCCAGCCA	189
Db	21	ThrCysAlaValTyrGlySerPheSerAsnTyrTyrTrpSerTrpIleArgGlnPro	40
QY	190	CCAGTAAAGGGTCTGGAGTGGATTGGTGAATCAATCATAGTGAAGCACCACCACTACAAC	249
Db	41	ProGlyLysGlyLeuGlnTrpValGlyGluLeuHisSerGlySerThrAsnTyrAsn	60
QY	250	CGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACAGTCCAAAGAACCACTTCTCTG	309
Db	61	ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu	80
QY	310	AACTGAGCTGTGACCGCTGCGACACGGCTGTGTATTAATCTGCGAGAGTAATTAAT	369
Db	81	LysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaArgValGlyLeu	100
QY	370	TGGTTC-----GACCCCTGGGCCAGGGAACC	396
Db	101	TyrTyrAspIleLeuThrGlyTyrTyrProSerGlyMetAspValTrpGlyLysGlyThr	120
QY	397	CTGGTCACCGTCTCTCA-----GCCTCAACCAAGGGC	429
Db	121	LeuValThrValSerSerGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly	140
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Job time : 26.264 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 11.9272 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
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Total number of hits satisfying chosen parameters: 525148

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=btosum62 -TRANS=human0.cdi  
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Database : Issued Patents AA:\*  
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4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	780	80.7	472	4	US-08-793-450-8
2	766.5	79.3	473	4	US-09-049-672A-4
3	739	76.4	476	3	US-08-487-550-12
4	722	74.7	476	3	US-08-487-550-4
5	700	72.4	467	4	US-08-523-894-8
6	700	72.4	467	4	US-08-523-894-10
7	700	72.4	467	4	US-08-523-894-12
8	622	64.3	116	3	US-08-545-809A-118
9	607.5	62.8	832	3	US-08-630-820-7
10	607	62.8	832	3	US-08-630-820-7
11	578	59.8	123	4	US-09-460-384-37
12	565	58.4	142	2	US-08-480-774A-2

13	564.5	58.4	273	3	US-08-397-411-6	Sequence 6, Appli
14	564.5	58.4	446	3	US-08-397-411-7	Sequence 7, Appli
15	560	57.9	260	4	US-09-171-945-93	Sequence 93, Appl
16	552	57.1	229	2	US-08-887-352B-20	Sequence 20, Appl
17	552	57.1	229	4	US-09-109-207C-20	Sequence 20, Appl
18	552	57.1	229	4	US-09-296-005-20	Sequence 20, Appl
19	552	57.1	233	2	US-08-887-352B-25	Sequence 25, Appl
20	552	57.1	233	4	US-09-109-207C-25	Sequence 25, Appl
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22	552	57.1	306	4	US-09-171-945-95	Sequence 95, Appl
23	552	57.1	451	2	US-08-887-352B-14	Sequence 14, Appl
24	552	57.1	451	2	US-08-887-352B-16	Sequence 14, Appl
25	552	57.1	451	3	US-08-466-151-65	Sequence 65, Appl
26	552	57.1	451	4	US-09-109-207C-14	Sequence 14, Appl
27	552	57.1	451	4	US-09-109-207C-16	Sequence 14, Appl
28	552	57.1	451	4	US-09-296-005-14	Sequence 16, Appl
29	552	57.1	451	4	US-09-296-005-16	Sequence 16, Appl
30	552	57.1	613	4	US-09-171-945-113	Sequence 113, App
31	550	56.9	116	3	US-08-545-809A-140	Sequence 140, App
32	546.5	56.5	716	4	US-09-171-945-125	Sequence 125, App
33	546	56.5	229	2	US-08-887-352B-21	Sequence 21, Appl
34	546	56.5	229	4	US-09-109-207C-21	Sequence 21, Appl
35	546	56.5	229	4	US-09-296-005-21	Sequence 21, Appl
36	546	56.5	233	2	US-08-887-352B-26	Sequence 26, Appl
37	546	56.5	233	4	US-09-109-207C-26	Sequence 26, Appl
38	546	56.5	233	4	US-09-296-005-26	Sequence 26, Appl
39	546	56.5	451	2	US-08-887-352B-18	Sequence 18, Appl
40	546	56.5	451	4	US-09-109-207C-18	Sequence 18, Appl
41	546	56.5	451	4	US-09-282-505-2	Sequence 2, Appli
42	546	56.5	451	4	US-09-054-255-2	Sequence 2, Appli
43	546	56.5	451	4	US-09-296-005-18	Sequence 18, Appl
44	539	55.7	118	3	US-08-545-809A-142	Sequence 142, App
45	538	55.6	116	3	US-08-545-809A-92	Sequence 92, Appl

#### ALIGNMENTS

RESULT 1  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHAABITHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT



Score: 722.00 Matches: 143  
Percent Similarity: 82.42% Conservative: 7  
Best Local Similarity: 78.57% Mismatches: 20  
Query Match: 74.66% Indels: 12  
DB: 3 Gaps: 3

US-08-728-463B-219 (1-524) x US-08-487-550-4 (1-476)

QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCTAGATGGGTCTGTCTCAG 72  
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTCACGCTACAGCAGTGGGGCGGAGCAGCTTGAAGCCTCGAGACCCCTGCTCCAC 132  
Db 21 ValLysLeuGlnTrpGlyGluGlyLeuLeuGlnProSerGluThrLeuSerArgThr 40

QY 133 TGGCGTGTCTATGTTCTCTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189  
Db 41 CysValValSerGlyGlySerIleSerGlyTyrTrpTrpTrpTrpLeuArgGlnThr 60

QY 190 CCAGGTAAGGCTGGAGTGGATTGGTGAATCAATCATAGTGA---AGCACCAACTAC 246  
Db 61 ProGlyArgGlyLeuGluTrpIleGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyr 80

QY 247 AACCGTCTCTCAAGAGTCAGTCACCATATCATAGTAGACACGTCACAGACCTGCTCT 306  
Db 81 AsnProSerLeuLysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhe 100

QY 307 CTGAACACTGAGCTGTGACCGCTGGGACACGCTGTGTATTACTGTGGAGA----- 360  
Db 101 LeuAsnLeuAsnSerValThrAspAlaSerThrAlaValTyrCysAlaArgGlyPro 120

QY 361 -----GTAATTAAATGGTTCCAGCCCTTGGGGCCAGGGAACC 396  
Db 121 ArgProAspCysThrThrIleCysTyrGlyGlyTrpValAspValTrpGlyProGlyAsp 140

QY 397 CTGCTCACCTCTCTCAGCTCAACCAAGGGCCCATCGCTCTTCCCGCTGGCACCTCC 456  
Db 141 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 160

QY 457 TCCAAGAGCACCTCTGGGGCCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCC 516  
Db 161 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 180

QY 517 GAACCG 522  
Db 181 GluPro 182

RESULT 5  
US-08-728-463B-219 (1-524) x US-08-487-550-4 (1-476)  
; Sequence 8, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-523-894-8

Alignment Scores:  
Pred. No.: 4,748-61 Length: 467  
Score: 700.00 Matches: 139  
Percent Similarity: 84.66% Conservative: 10  
Best Local Similarity: 78.98% Mismatches: 21  
Query Match: 72.39% Indels: 6  
DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x US-08-523-894-8 (1-467)

QY 13 ATGAACACCTGGTTCCTCTCTCTGGTGGCAGCTCTAGATGGGTCTGTCTCAG 72  
Db 1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20

QY 73 GTCACGCTACAGCAGTGGGGCGGAGCAGCTTGAAGCCTCGAGACCCCTGCTCCAC 132  
Db 21 ValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

QY 133 TGGCGTGTCTATGTTCTCTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCA 189  
Db 41 CysSerValSerGlyGlySerIleSerGlyAspTyrTrpTrpTrpTrpLeuArgGlnSer 60

QY 190 CCAGGTAAGGCTGGAGTGGATTGGTGAATCAATCATAGT---GGAAGCACCAACTAC 246  
Db 61 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyr 80

QY 247 AACCGTCTCTCAAGAGTCAGTCACCATATCATAGTAGACACGTCACAGACCTGCTCT 306  
Db 81 AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100

QY 307 CTGAACACTGAGCTGTGACCGCTGGGACACGCTGTGTATTACTGTGG----- 357  
Db 101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrCysAlaSerAsnIle 120

QY 358 --AGAGTAATTAATTTGGTTCCAGCCCTTGGGGCCAGGAAACCTGTGCTCCTCTCA 414  
Db 121 LeuLysTyrLeuHisTrpLeuLeuTyrTrpGlyGlnGlyValLeuValThrValSer 140

QY 415 GCCTCAACCAAGGGCCCATCGGTCTTCCCGCTGGACCCCTCTCCAGAGACACTCTGG 474  
Db 141 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 160

QY 475 GGCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCG 522  
Db 161 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 176

RESULT 6  
US-08-523-894-10  
; Sequence 10, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy

190	CCAGGTAAAGGCTCTGGAGTGGTGAATC-----AATCATAGTGGAGGACCAACATAC	246
61	ProGlyLysGlyLeuGluTrrPileGlySerPheTyrSerSerGlyAsnThrTyrTyr	80
247	AACCCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACACAGTTCTCT	306
81	AsnProSerLeuLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer	100
307	CTGAAACTGAGCTCTGTACACCGCTCGGACACGGCTGTGTATTACTGTGCGGAGA-----	360
101	LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysValArgAspArg	120
361	-----GTAATT-----AATGGTTTCACCCCTGGGGCCAGGGAACC	396
121	LeuPheSerValValGlyMetValTyrAsnAsnTrpPheAspValTrrPglyProGlyVal	140
397	CTGGTCAACCGTCTCCTCAGCCTCAACGAGGGCCATCGGTCTTCCCCCTGGCACCCCTCC	456
141	LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer	160
457	TCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCGTGCTCAAGGACTACTTCCCC	516
161	SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro	180
517	GAACCG	522
181	GluPro	182

RESULT 4  
 US-08-487-550-4  
 ; Sequence 4, Application US/08487550  
 ; Patent No. 6113898  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Darrell R.  
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF,  
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 ; STREET: 699 Prince Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:

```

; REFERENCE/DOCKET NUMBER: 0127113-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-4

Alignment Scores:
Pred. No.: 3,236-63 Length: 476

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	247	AACCGCTCTCTCAAGAGTCGAGTCCACCATATCAGTAGACAGCTCCCAAGAACCAAGTTCTCT	306
Qy		:::::	
	81	AsnProSerLeuAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer	100
Db		:::::	
	307	CTGAACACTGAGCTCTGTGCACCGCTCGCGACACGGCTGTATTACTGTGGC-----	357
Qy		:::::	
	101	LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrCysAlaSerAsnIle	120
Db		:::::	
	358	---AGAGTAATTAATGTGTTCGACCCTTGCGGCCGAGGAACCTGTGCACCGTCTCTCA	414
Qy		:::::	
	121	LeuLysTyrLeuHisTrpLeuLeuTyrTrpGlyGlnGlyValLeuValThrValSerSer	140
Db		:::::	
	415	GCTCCAACAAGGGCCCATCGTCTTCCCCTGTGCACCCCTCTCCAAGAGCACCTCTGGG	474
Qy		:::::	
	141	AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu	160
Db		:::::	
	475	GGCA CAGCGGCGCTGGGTGCTGGTCAAAGCACTTCCCCAAACCG	522
Qy		:::::	
	161	SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro	176
Db		:::::	

## RESULT 8

US-08-545-809A-118  
; Sequence 118, Application US/08545809A

Patent No. 6096878  
GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko

	TITLE OF INVENTION:	HUMAN IMMUNOGLOBULIN VH GENE
	TITLE OF INVENTION:	SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street

CITY: Boston  
 STATE: MA

STATE: FR  
COUNTRY: US  
ZIP: 02110-2804

REF: 02110-2004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

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; MEDIUM TYPE: DISKETTE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95

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```
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: FastSEQ for Windows Vers
; CURRENT APPLICATION DATA:
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/
; FILING DATE: 27-MAR-199
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FILING DATE: 27-MAR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP93/00603

; AFFILIATION NUMBER: FCI/  
 ; FILING DATE: 10-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066

REGISTRATION NUMBER: 25,080  
REFERENCE/DOCKET NUMBER: 06  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-50  
TELEFAX 617-542-8906

TELEFAX: 817-342-8908  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 118:

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; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids

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; LENGTH: 118 amino acid
; TYPE: amino acid
; TOPOLOGY: linear

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MOLECULE TYPE:  
US-08-545-809A-118



Score: 607.50 Matches: 121  
Percent Similarity: 85.44% Conservative: 14  
Best Local Similarity: 76.58% Mismatches: 16  
Query Match: 62.82% Indels: 7  
DB: 3 Gaps: 4

US-08-728-463B-219 (1-524) x US-08-630-820-7 (1-832)

QY 70 CAGGTGACAGTACAGAGTGGGGCGGAGGACTGTTGAAGCTTCGAGACCCCTGCTCCTC 129  
Db 2 GluValGlnLeuGlnGluSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeu 21  
QY 130 ACCTGCGCTCTATGCTGCTTCTCTC---AGTGGTTACTACTGGAGCTGGATCCGCCAG 186  
Db 22 ThrCysThrValSerGlyPheThrIleSerSerGlyTyrSerTrpHisTrpValArgGln 41  
QY 187 CCACAGGTGAAGGCTGAGGTGAGTGGTGAATCAATCATAGTGAAGCACTAC 246  
Db 42 ProProGlyArgGlyLeuGlnTrpIleGlyTyrIleGlnTyrSerGlyIleThrAsnTyr 61  
QY 247 AACCGTCTCTCAAGAGTGGAGTACCATATCATAGTACAGACGTCGAGAACCGTTCTCT 306  
Db 62 AsnProSerLeuLysSerArgValThrMetLeuValAspThrSerLysAsnGlnPheSer 81  
QY 307 CTGAAGTCTGAGTCTGACCGCTGCGGACGCGCTGTGTATTACTGTCGAGGTA--- 363  
Db 82 LeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGluAsp 101  
QY 364 -----ATTAATGG---TTGACACCTTGGGGCGGAGAACCTG-----GTCACCGTC 408  
Db 102 TyrAspTyrHisTrpTyrPheAspValTrpGlyGlnGlySerLeuValThrValThrVal 121  
QY 409 TCTCAGCTCAACCAAGGCCCATCGGTCTTCCCTGCGACCCCTCTCCCAAGACAC 468  
Db 122 SerSerAlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThr 141  
QY 469 TCTGGGGCACGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGACCG 522  
Db 142 SerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro 159

RESULT 10  
US-08-728-463B-219 (1-524) x US-08-630-820-7 (1-832)  
; Sequence 37, Application US/09460384  
; Patent No. 6337316  
; GENERAL INFORMATION:  
; APPLICANT: EL TAYAR, Nabil  
; BLECHNER, Steven  
; JAMESON, Brad  
; TEPPER, Mark  
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,  
; SAME  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/460,384  
; FILING DATE: 13-Dec-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/12312  
; FILING DATE: 11-JUN-1998  
; APPLICATION NUMBER: US 60/049,470

FILING DATE: 12-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: EL TAYAR=1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-460-384-37

Alignment Scores:  
Pred. No.: 5,6e-52 Length: 219  
Score: 607.00 Matches: 121  
Percent Similarity: 86.99% Conservative: 6  
Best Local Similarity: 82.88% Mismatches: 17  
Query Match: 62.77% Indels: 2  
DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x US-09-460-384-37 (1-219)

QY 91 GCGCGAGGAGCTGTTGAAGCTTCGAGACCCCTGCTCCCTCACCTGCGCTCTCTATGGTGT 150  
Db 2 GlyProGlyLeuValLysProSerGluAlaLeuSerLeuThrCysThrValSerGlyAsp 21  
QY 151 TCCTTCAGTGGT-----TACTACTGGAGCTCGATCCGCCAGCCACAGGTAAAGGTCTG 204  
Db 22 SerIleAsnThrIleLeuTyrTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeu 41  
QY 205 GAGTGGATTGGTGAATCAATCATAGTGAAGCACTACACCCGCTCTCTCAAGAGT 264  
Db 42 GluTrpIleGlyTyrIleTyrSerGlySerThrTyrGlyAsnProSerLeuLysSer 61  
QY 265 CGAGTCACCATATCAGTAGACACACGCTCCCAAGAACCACTCTCTCTGAAACTGAGCTCTGTG 324  
Db 62 ArgValThrIleSerValAsnThrSerLysAsnGlnPheTyrSerLysLeuSerVal 81  
QY 325 ACCGCTGCGGACACGCTGTGTATTACTGTGCGAGAGTAATTAATGGTTCGACCCCTGG 384  
Db 82 ThrAlaAlaAspThrAlaValTyrTyrCysAlaAsgValProLeuValValAsnProTrp 101  
QY 385 GCGCAGGAGAACCTGGTCAACCTCTCTCAGCTCAACCAAGGCCCATCGGTCTTCCCC 444  
Db 102 GlyGlnGlyThrLeuValThrValSerSerAlaSerThrLysGlyProSerValPhePro 121  
QY 445 CTGGCACCTCTCTCAAGAGACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAG 504  
Db 122 LeuAlaProSerSerLysSerThrSerGlyThrAlaAlaLeuGlyCysLeuValLys 141  
QY 505 GACTACTTCCCGAACCG 522  
Db 142 AspTyrPheProGlnPro 147

RESULT 11  
US-08-793-450-4  
; Sequence 4, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHAABIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:

ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-4

Alignment Scores:  
Pred. No.: 3,436-49 Length: 123  
Score: 578.00 Matches: 109  
Percent Similarity: 90.24% Conservative: 2  
Best Local Similarity: 88.62% Mismatches: 4  
Query Match: 59.77% Indels: 8  
DB: 4 Gaps: 1

US-08-728-463B-219 (1-524) x US-08-793-450-4 (1-123)

Qy 70 CAGGTGAGTACAGCAGTGGCGGAGGACTGTGAAGCTTCGGAGACCTGTCCCTC 129  
Db 1 GlnValGlnLeuGlnTrpGlyAlaGlyLeuLeuLysProSerGluThrLeuSerLeu 20  
Qy 130 ACCTGCGCTCTATGCTGCTTCCTTCAGTGGTACTACTGGAGCTGGATCCCGAGCCA 189  
Db 21 ThrCysThrValTyrGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPro 40  
Qy 190 CCAGGTAAAGGCTTGGAGTGGATTGGTGAATCAATCATAGTGAAGACCAACTACAAC 249  
Db 41 ProGlyLysGlyLeuGluTrpIleGlyGluIleAsnHisSerGlySerThrAsnTyrAsn 60  
Qy 250 CCGTCTCTCAAGAGTGGAGTACCATATCAGTACAGACAGTCCAGAACACCGTCTCTCTG 309  
Db 61 ProSerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80  
Qy 310 AAAGTGAAGTCTGAGCGCTGGAGCAGCGCTGTGTATTACTGTGGAGAGTAAT--- 366  
Db 81 LysLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAlaProGlu 100  
Qy 367 -----AATTGTTCCAGCCTTGGGCGCCAGGAAACCTGTGTCACC 405  
Db 101 TyrLysTrpLysTyrHisGlyAspTrpPheAspProTrpGlyGlnGlyThrThrValThr 120  
Qy 406 GTCTCTCA 414  
Db 121 ValSerSer 123

RESULT 12

US-08-480-774A-2  
Sequence 2, Application US/08480774A  
Patent No. 5852186  
GENERAL INFORMATION:  
APPLICANT: MARASCO, Wayne A.  
APPLICANT: SODOSKI, Joseph G.  
APPLICANT: HAZELTINE, William A.  
APPLICANT: POSNER, Marshall R.  
TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN  
TITLE OF INVENTION: ANTI-9P 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME  
TITLE OF INVENTION: AND USE THEREOF  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,774A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/400,674  
FILING DATE: 08-MAR-1995  
APPLICATION NUMBER: 07/804,652  
FILING DATE: 10-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41450-FWC-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 142 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-480-774A-2

Alignment Scores:  
Pred. No.: 6,838-48 Length: 142  
Score: 565.00 Matches: 110  
Percent Similarity: 85.92% Conservative: 12  
Best Local Similarity: 77.46% Mismatches: 12  
Query Match: 58.43% Indels: 8  
DB: 2 Gaps: 2

US-08-728-463B-219 (1-524) x US-08-480-774A-2 (1-142)

Qy 13 ATGAACACCTGTGTTCTTCTCTCTCTGTCGAGCTCTAGATGGTCTGTCTCAG 72  
Db 1 MetGluHisLeuTrpPheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
Qy 73 GTCAGCTACAGCAGTGGCGGCGAGGACTGTGAAGCTTCGGAGACCTGTCCCTCACC 132  
Db 21 ValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40  
Qy 133 TGCCTGTCTATGTTGTTCTCTCAGTGGTGTACTGAGCTGATCCGCGCAGCCACA 192  
Db 41 CysThrValSerGlyGlySerIleSerHisTyrTrpSerTrpIleArgGlnSerPro 60

QY 193 GCTAGGCTCGAGTGGATTGGTGAATCAATCATAGTGGAGACCACTACACCG 252  
Db 61 GlyLysGlyLeuGlnTrpLeuGlyTyrIleTyrTyrSerGlySerThrAsnTyrSerPro 80  
QY 253 TCTCTCAAGAGTCGAGTCACCATATCAGTAGACACCTCCAAAGAACAGTTCTCTCTGAAA 312  
Db 81 SerLeuLysSerArgValThrIleSerValGluThrSerLysAsnGlnPheSerLeuLys 100  
QY 313 CTGAGCTCTGTGACCGCTCGGACACGCGTGTGTATTACTGTGCGAGA----- 360  
Db 101 LeuThrSerMetThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyProValPro 120  
QY 361 GTAATTAATGG-----TTTCGACCCCTTGGGGCCAGGACCCCTGTGTCCCGNC 408  
Db 121 AlaValPheTyrGlyAspTyrArgLeuAspProTrpGlyGlnGlyThrLeuValThrVal 140  
QY 409 TCCTCA 414  
Db 141 SerSer 142  
RESULT 13  
US-08-397-411-6  
; Sequence 6, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2420  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-6  
Alignment Scores:  
Pred. No.: 9.21e-48 Length: 273  
Score: 564.50 Matches: 115  
Percent Similarity: 81.58% Conservative: 9  
Best Local Similarity: 75.66% Mismatches: 27  
Query Match: 58.38% Indels: 1

DB: 3 Gaps: 1  
US-08-728-463B-219 (1-524) x US-08-397-411-6 (1-273)  
QY 70 CAGGTGACAGCTACAGCAGTGGGGCCAGGACCTGTGTAAGCCCTTCGAGACCCCTGTCCCTC 129  
Db 1. GlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20  
QY 130 ACCTCGCTGTCTATGTGGTTCCTTTCAGTGGTTACTACTGAGCTGGATCCGCCACCA 189  
Db 21 ThrCysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnSer 40  
QY 190 CCAGTAAGGCTCGAGTGGATTGGTGAATCAATCATAGTGGAGACCACTACACCA 249  
Db 41 ProGlyLysGlyLeuGlnTrpLeuGlyValLysTrpSerGlyGlySerThrGluTyrAsn 60  
QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACCTCCAAAGAACAGTTCTCTCTG 309  
Db 61 AlaAlaPheIleSerArgLeuThrIleSerLysAspThrSerLysAsnGlnValSerLeu 80  
QY 310 AAATGAGCTCTGTGACCGCTCGGACACGCGTGTGTATTACTGTGCGAGAGTAAAT 369  
Db 81 LysLeuAsnSerLeuThrAlaAlaAspThrAlaValTyrTyrCysAlaArgAsnAspArg 100  
QY 370 TGG---TTTCGACCCCTTGGGGCCAGGACCCCTGTGTAAGCCCTTCGAGACCCCTCAAC 426  
Db 101 TyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThrLys 120  
QY 427 GSCCATCGTCTTCCCTCGCACCCCTCTCCAAAGAGCACCTCTGGGGGCGACAGCGGC 486  
Db 121 GlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyThrAlaAla 140  
QY 487 CTGGGCTGCTGCTCAAGAGTACTTCCCGCAACCG 522  
Db 141 LeuGlyCysLeuValLysAspTyrPheProGluPro 152  
RESULT 14  
US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2420  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-6

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; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-7

Alignment Scores:
Pred. No.: 1,06e-47 Length: 446
Score: 564.50 Matches: 115
Percent Similarity: 81.58% Conservatives: 9
Best Local Similarity: 75.66% Mismatches: 27
Query Match: 58.38% Indels: 1
DB: 3 Gaps: 1

US-08-728-463B-219 (1-524) x US-08-397-411-7 (1-446)
QY 70 CAGGTGACGCTACAGCAGTGGGCGCAGGACTGTGAAGCCTTCGGAGACCCCTGTCCTC 129
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 20
QY 130 ACTGCGCTGTCTAAGTGTTCCTTCAGCTGGTTACTACTGGAGCTGGATCCCGCCAGCCA 189
Db 21 ThrCysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnSer 40
QY 190 CCAGTAAAGGTCTGGAGTGGATGGTGAATCAATCATAGTGGAGCACAACACTACAAC 249
Db 41 ProGlyLysGlyLeuGluTrpIleGlyValLysTrpSerGlyGlySerThrGluTyrAsn 60
QY 250 CCGTCTCTCAAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAGAACCACTCTCTCTG 309
Db 61 AlaAlaPheIleSerArgLeuThrIleSerLysAspThrSerLysAsnGlnValSerLeu 80
QY 310 AAAGTACGCTGTGACCGCTGGCGGACACGCTGTGTATTACTGTGCGAGAGTAATTAAT 369
Db 81 LysLeuAsnSerLeuThrAlaAlaAspThrAlaValTyrCysAlaArgAsnAspArg 100
QY 370 TGG---TTCCACCTTCGGGCGCCAGGAACTCTGTACACCTCTCTCAGCTCAACCAAG 426
Db 101 TyrAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerAlaSerThrLys 120
QY 427 GGCCATCGCTTTCCTCCCTGGCACCTCTCTCAAGAGACCTCTCTGGGGGCACAGCGGCC 486
Db 121 GlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAla 140
QY 487 CTGGGCTGCTGTCTAAGGACTACTTCCCGAACC 522
Db 141 LeuGlyCysLeuValLysAspTyrPheProGluPro 152

RESULT 15
US-09-171-945-93
; Sequence 93, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 93
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-93

Alignment Scores:
Pred. No.: 2,52e-47 Length: 260
Score: 580.00 Matches: 114
Percent Similarity: 75.14% Conservatives: 16
Best Local Similarity: 65.90% Mismatches: 37
Query Match: 57.91% Indels: 6
DB: 4 Gaps: 3

US-08-728-463B-219 (1-524) x US-09-171-945-93 (1-260)
QY 22 CTGTGTTTC---TTCCTCTCTCTGTGGCAGCTCTCTAGATGGTCTCTCAGGTGCAG 78
Db 3 LeuTrpLeuAsnTrpIlePheLeuValThrLeuLeuAsnGlyIleGlnCysGluValGln 22
QY 79 CTACACAGTGGGGCGCAGGACTGTGAAGCCTTCGGAGACCCCTGTCTCTCACCCTCGCT 138
Db 23 LeuGlnGlnSerGlyProGlyLeuValArgProSerGlnThrLeuSerLeuThrCysThr 42
QY 139 GTCTATGGTGGTTCCTTCAGTGGTTACTACTCGAGCTGGATCCGCCAGCCACCAGTAAG 198
Db 43 AlaSerGlyPheAsnIleLysAspAsnTyrMetHisTrpValArgGlnProProGlyArg 62
QY 199 GGTCTGAGTGGATTGGTGAATCAAT---CATAGTGAAGCACCACCACTCAACCCGTCT 255
Db 63 GlyLeuGluTrpIleGlyTrpIleAspProGluAsnGlyAspThrGluTyrAlaProLys 82
QY 256 CTCACAGTGGAGTCCACCATATCAGTAGACACGTCACAGACCCAGTCTCTCTGAAACTG 315
Db 83 PheArgGlyArgValThrMetLeuAlaAspThrSerLysAsnGlnPheSerLeuArgLeu 102
QY 316 AGTCTGTGACCGCTCGGCACACGCTGTGTATTACTGTGCGAGAGTAATTAAT----- 369
Db 103 SerSerValThrAlaAlaAspThrAlaValTyrCysHisValLeuIleTyrAlaGly 122
QY 370 -----TGTTTCGACCTTTGGGGCCAGGAACTCTCTCAGCTCTCTCAGCCTCAACC 423
Db 123 TyrLeuAlaMetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSerAlaSerThr 142
QY 424 AAGGGCCCATCGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGGGGCACAGCG 483
Db 143 LysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAla 162
QY 484 GCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACC 522
Db 163 AlaLeuGlyCysLeuValLysAspTyrPheProGluPro 175
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Search completed: June 3, 2003, 09:47:34  
Job time : 14.9272 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 17.7656 Seconds  
(without alignments)  
4545.477 Million cell updates/sec

Title: US-08-728-463B-220  
Perfect score: 761  
Sequence: 1 AGCTTGCCACCATGATGTT.....TGGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2 1/USPTO.spool/US08728463/runat\_03062003\_085615\_16827/app.query.fasta\_1.3690  
-DB=PIR 73 -QMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0  
-UNITS=bits START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1 1 177 @runat\_03062003\_085615\_16827 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 73:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	621	81.6	130	2	S40368
2	592	77.8	141	2	A49134
3	590	77.5	125	2	S40333
4	587	77.1	125	2	S40316
5	586	77.0	132	2	S40334
6	581	76.3	127	2	S40367
7	580	76.2	117	2	S21527
8	574	75.4	117	2	S46376
9	571	75.0	131	2	S40352
10	570	74.9	129	2	S40369
11	564	74.1	125	2	S40349
12	562	73.9	123	2	S40331
13	562	73.9	128	2	S46372
14	558.5	73.4	124	2	S40336
					Ig kappa chain - h
					Ig kappa chain V-I
					Ig kappa chain V-J
					Ig kappa chain - h
					Ig kappa chain - h
					Ig kappa chain V-J
					Ig kappa chain pre
					Ig kappa chain V-J
					Ig kappa chain V-J
					Ig kappa chain - h
					Ig kappa chain - h
					Ig kappa chain V-J
					Ig kappa chain var
					Ig kappa chain V-J

15	557	73.2	132	2	S38646	Ig kappa chain V r
16	556	73.1	127	2	S11240	Ig kappa chain V r
17	553	72.7	129	2	S52793	Ig kappa chain V r
18	550	72.3	125	2	S40353	Ig kappa chain V-J
19	550	72.3	126	2	S40335	Ig kappa chain V-J
20	549	72.1	129	1	K1HUKK	Ig kappa chain pre
21	548	72.0	124	2	S40318	Ig kappa chain V r
22	546	71.7	129	2	S40317	Ig kappa chain - h
23	546	71.7	139	2	S40365	Ig kappa chain - h
24	545	71.6	129	2	S52789	Ig kappa chain V r
25	540.5	71.0	129	2	S40332	Ig kappa chain - h
26	537	70.6	123	2	S40313	Ig kappa chain V-J
27	535	70.3	129	2	S52792	Ig kappa chain V r
28	533.5	70.1	125	2	S40315	Ig kappa chain - h
29	533.5	70.1	135	2	S24320	Ig kappa chain pre
30	531	69.9	117	2	S46371	Ig kappa chain V-J
31	531	69.8	117	1	K1HUL2	Ig kappa chain pre
32	528	69.4	117	2	B21056	Ig kappa chain pre
33	526.5	69.2	120	2	S46374	Ig kappa chain V-J
34	526	69.1	117	2	S24206	Ig kappa chain V r
35	523	68.7	117	1	K1HUL1	Ig kappa chain pre
36	522	68.6	117	2	S11700	Ig kappa chain pre
37	521	68.5	117	2	S41809	Ig kappa chain V r
38	521	68.5	122	2	S40314	Ig kappa chain - h
39	520	68.3	117	2	C21056	Ig kappa chain pre
40	520	68.3	122	2	S40370	Ig kappa chain - h
41	517.5	68.0	122	2	S40351	Ig kappa chain V-J
42	516	67.8	120	2	S46370	Ig kappa chain V-J
43	514	67.5	117	2	S41810	Ig kappa chain V r
44	513	67.4	116	2	A27594	Ig kappa chain pre
45	509	66.9	125	2	S40350	Ig kappa chain - h

#### ALIGNMENTS

##### RESULT 1

S40368  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40368  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40368  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-130 <KLE>  
A;Cross-references: EMBL:X72478; NID:g441424; PIDN:CAA51146.1; PID:g441425  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:		Pred. No.:	1.28e-46	Length:	130
Score:		Percent Similarity:	621.00	Matches:	118
Best Local Similarity:		Query Match:	94.62%	Conservative:	5
Query Match:		DB:	90.77%	Mismatches:	7
			81.60%	Indels:	0
			2	Gaps:	0
US-08-728-463B-220 (1-420) x S40368 (1-130)					
Qy	22	CCAGCTCAGCTCCTCGGTCCTCGTCTGGTCTCCAGGTTCCAGATCCGACATCCAG	81		
Db	1	ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCysAspIleGln	20		
Qy	82	ATGACCCAGCTCTCCATCTTCCGTCGTCTGTCATCTGTAGGAGACAGAGTCACCATCTGT	141		
Db	21	MetThrGlnSerProSerValSerAlaSerValGlyAspArgValIleThrCys	40		
Qy	142	CGGGCGAGTCAGGATATTAGCAGCTGGTGTAGCTGTATGATGATTAACCCAGGTAAGCA	201		









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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-131 <KLE>
A;Cross-references: EMBL:X72462; NID:g441392; PIDN:CAA51130.1; PID:g441393
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.08e-42 Length: 131
Score: 571.00 Matches: 110
Percent Similarity: 92.31% Conservative: 10
Best Local Similarity: 84.62% Mismatches: 10
Query Match: 75.03% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x S40352 (1-131)
QY 13 ATGATGTCCTCCAGCTCCTCGGTCCTCTGCTCTCCAGGTTCCAGATGC 72
Db 1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProAspThrLysCys 20
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTCTGTCATCTGTAGGAGACAGATCACC 132
Db 21 AspIleGlnMetThrGlnSerProSerSerLeuLeuLeuLeuLeuValGlnGlnLysPro 60
QY 133 ATCACTTTGCGCGAGTCAGATATAGCAGCTGGTTCAGCTGGTTCAGCATAAACA 192
Db 41 IleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 60
QY 193 GGTAAAGCCTAAGCTCTGATCTATGTCGTCATCCAGTTCGATCCAGTTGGAAAGTGTGCCATCA 252
Db 61 GlyLysValProLysLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 80
QY 253 AGTTTCAGCGGAGTGTGATCTGGACAGATTCACCTCTCACCATCAGCAGCCTGCAGCCT 312
Db 81 ArgPheSerGlySerGlySerGlyThrAspPheSerLeuThrIleSerLeuGlnPro 100
QY 313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
Db 101 GluAspValAlaThrTyrTyrCysGlnLysTyrAsnSerValProArgThrPheGlyGln 120
QY 373 GGAACCAAGCTGGAGATCAACGAAGTGTG 402
Db 121 GlyThrLysValGluIleLysArgThrVal 130

RESULT 10
S40369
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40369
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.77e-42 Length: 129
Score: 570.00 Matches: 112
Percent Similarity: 92.19% Conservative: 6
Best Local Similarity: 87.50% Mismatches: 10
Query Match: 74.90% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x S40369 (1-129)
QY 13 ATGATGTCCTCCAGCTCCTCGGTCCTCTGCTCTCCAGGTTCCAGATGC 72
Db 2 MetArgValLeuAlaGlnLeuLeuGlyLeuLeuLeuLeuCysPheProGlyAlaArgCys 21
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTCTGTCATCTGTAGGAGACAGATCACC 132
Db 22 AspIleGlnMetThrGlnSerProSerSerLeuLeuLeuLeuLeuValGlnGlnLysPro 41
QY 133 ATCACTTTGCGCGAGTCCAGATATAGCAGCTGGTTCAGCTGGTTCAGCATAAACA 192
Db 42 IleThrCysArgAlaSerHisValIleSerAsnHisLeuValTrpPheGlnGlnLysPro 61
QY 193 GGTAAAGCCTAAGCTCTGATCTATGTCGTCATCCAGTTCGATCCAGTTGGAAAGTGTGCCATCA 252
Db 62 GlyLysAlaProLysSerLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 81
QY 253 AGTTTCAGCGGAGTGTGATCTGGACAGATTCACCTCTCACCATCAGCAGCCTGCAGCCT 312
Db 82 LysPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerLeuGlnPro 101
QY 313 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372
Db 102 GluAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyrProTyrThrPheGlyGln 121
QY 373 GGAACCAAGCTGGAGATCAACGA 396
Db 122 GlyThrLysLeuGluIleLysArg 129

RESULT 11
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.27e-41 Length: 125
Score: 564.00 Matches: 109
Percent Similarity: 92.80% Conservative: 7
Best Local Similarity: 87.20% Mismatches: 9
Query Match: 74.11% Indels: 0
DB: 2 Gaps: 0

US-08-728-463B-220 (1-420) x S40349 (1-125)
QY 22 CAGCTCAGCTCCTCGGTCCTCGGTCCTCTGCTCTCCAGGTTCCAGATGCAGATCCAG 81
Db 1 ProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArgCysAlaIleGln 20
QY 82 ATGACCCAGTCTCCATCTTCCTGCTCTGTCATCTGTAGGAGACAGATGCACATCCTGT 141
Db 21 LeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCys 40
QY 142 CGGCGGAGTCAGATATAGCAGCTGGTTCAGCTGGTTCAGCATAAACAAGGATAAGCA 201
Db 41 ArgAlaSerGlnGlyIleSerSerAlaLeuAlaTrpTyrGlnGlnLysProGlyLysAla 60
QY 202 CCTAAGCTCTGATCTATGCTGATCCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAG 261
Db 202 CCTAAGCTCTGATCTATGCTGATCCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAGTTTGCAG
```

Db 61 ProLysLeuLeuLeuTyrAspAlaSerSerLeuGluSerGlyValProSerArgPheSer 80  
QY 262 GGAAGTGGATCGGACAGATTTCCTCACCATCAGCAGCTCGAGCTCGAAGATTTT 321  
Db 81 GlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100  
QY 322 GCAACTTACTATTGCAACAGGCTAATAGTTTCCCGTACACTTTGGTCAGGAACCAAG 381  
Db 101 AlaThrTyrTyrCysGlnGlnPheAsnThrTyrProLeuThrPheGlyGlyThrLys 120  
QY 382 CTGGAGATCAAAACA 396  
Db 121 ValGluIleLysArg 125

## RESULT 12

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40331

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

S:J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 &lt;KLE&gt;

A:Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:g441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	1	91e-41	Length:	123
Score:	562.00	Matches:	110	
Percent Similarity:	93.50%	Conservative:	5	
Best Local Similarity:	89.43%	Mismatches:	8	
Query Match:	73.85%	Indels:	0	
DB:	2	Gaps:	0	

US-08-728-463B-220 (1-420) x S40331 (1-123)

QY 25 GCTCAGCTCCCTCGTCTCTGCTCTCGTTCCTCGTTCCTCGATCCGATCCAGATG 84  
Db 1 AlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuArgGlyAlaArgCysAspIleGlnMet 20  
QY 85 ACCAGTCTCCATCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 144  
Db 21 ThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThrIleThrCysArg 40  
QY 145 GCGAGTCAGGATATAGCAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCT 204  
Db 41 AlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaPro 60  
QY 205 AAGCTCCTGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264  
Db 61 LysLeuLeuLeuTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSerGly 80  
QY 265 ATGGATCTGGACAGATTTCTCTCACCATCAGCAGCTCGAGCTGCAAGATTTTGA 324  
Db 81 SerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAla 100  
QY 325 ACTTACTATTGTCACAGGCTAATAGTTTCCCGTACACTTTGGTCAGGAACCAAGCTG 384  
Db 101 ThrTyrTyrCysGlnGlnSerTyrSerProArgThrPheGlyGlnGlyThrLysVal 120  
QY 385 GAGATCAAA 393  
Db 121 GluIleLys 123

## RESULT 13

S46372

Ig light chain variable region (VJ) - human

C:Species: Homo sapiens (man)

C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: S46372

R:Bensimon, C.; Chaatagner, P.; Zouali, M.

S:EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re-

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46372

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 &lt;BEN&gt;

A:Cross-references: EMBL:Z27173

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:36-110/Domain: immunoglobulin homology &lt;IMM&gt;

## Alignment Scores:

Pred. No.:	1	9e-41	Length:	128
Score:	562.00	Matches:	109	
Percent Similarity:	91.41%	Conservative:	8	
Best Local Similarity:	85.16%	Mismatches:	11	
Query Match:	73.85%	Indels:	0	
DB:	2	Gaps:	0	

US-08-728-463B-220 (1-420) x S46372 (1-128)

QY 13 ATGATGGTCCCGATCCAGCTCCTCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 72  
Db 1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20  
QY 73 GACATCCAGATCACCAGCTCCTCATCTTCCGTCCTGTCATCTGTAGGAGACAGAGTCACC 132  
Db 21 AlaIleArgIleThrGlnSerProSerSerLeuSerAlaSerThrGlyAspArgValThr 40  
QY 133 ATCATTGTGCGGCGAGTCAGGATATTAGCAGCTGTTAGCTGTTAGCTGTTAGCTGTTAGCT 192  
Db 41 IleThrCysArgAlaSerGlnGlyIleSerSerTyrLeuAlaTrpTyrGlnGlnLysPro 60  
QY 193 GGTAAAGACACCTAAGCTCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252  
Db 61 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 80  
QY 253 AGTTTACCGGAGTGGATCTGGACAGATTTCTCCTCACCATCAGCAGCTGCGAGCT 312  
Db 81 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer 100  
QY 313 GAAGATTTTGCACACTTACTATTGTCACAGCTAATAGTTTCCCGTACACTTTTGGTCAG 372  
Db 101 GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerTyrProArgThrPheGlyGln 120  
QY 373 GGAACCAAGCTGGAGATCAAAACA 396  
Db 121 GlyThrLysValGluIleLysArg 128

RESULT 14  
S40336  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40336  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
S:J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40336  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-124 <KLE>  
A:Cross-references: EMBL:X72446; NID:9441360; PIDN:CAA51114.1; PID:g441361  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-105/Domain: immunoglobulin homology <IMM>

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Db	25	AlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArgValThr	44
Qy	133	ATCACTTGTGGGGCAGTCAGGATATTAGCAGCTGGTGGTTCATCAGCATAAACCA	192
Db	45	IleThrCysArgAlaSerGlnGlyIleSerSerTyrLeuAlaTptyrGlnGlnLysPro	64
Qy	193	GGTAAAGCACCTTAAGCTCCTGATCTATGCTGCATCCAGTTGCAAGTGGTGTCCCATCA	252
Db	65	GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer	84
Qy	253	AGGTTTCAGCGGAAGTGATCTGGGACAGATTTCCTCCTCACCATCAGACAGCTGCAGCCT	312
Db	85	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer	104
Qy	313	GAAGATTTTGCACCTTACTATTGTCAACAGAGCTAATAGTTTCCGTACACTTTTGGTCAG	372
Db	105	GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerTyrProArgThrPheGlyGln	124
Qy	373	GAACCAAGCTGGAGATCAAAACGA	396
Db	125	GlyThrLysValGluIleLysArg	132

Search completed: June 3, 2003, 09:08:01  
Job time : 19.7656 secs

Alignment Scores:			
Pred. No.:	5.17e-41	Length:	132
Score:	557.00	Matches:	108
Percent Similarity:	90.62%	Conservative:	8
Best Local Similarity:	84.38%	Mismatches:	12
Query Match:	73.19%	Indels:	0
DB:	2	Gaps:	0
US-08-728-463B-220 (1-420) x S38646 (1-132)			
Qy	13	ATGATGGTCCAGCTCAGCTCCGTCTCCTGCTGCTGCCAGGTTCCAGATGC	72
Db	5	MetargValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaArgCys	24
Qy	73	GACATCCAGATGACCCAGTCTCCATCTTCGGTCTCTGCATCTCTAGGAGACAGAGTCA	132

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 7.96662 Seconds  
(without alignments)  
4373.264 Million cell updates/sec

Title: US-08-728-463B-220  
Perfect score: 761  
Sequence: 1 AGCTTGCCACCATGATGTT.....TGCTGCACCATCTGCTTC 420

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO.spool/US08728463/runat\_03062003\_085614\_16804/app\_query.fasta\_1.3690  
-DB=SwissProt\_40 -OPWT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1.1 76 @runat\_03062003\_085614\_16804 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	72.1	129	1 KVIW HUMAN	P04431 homo sapien
2	531	69.8	117	1 KVIJ HUMAN	P01602 homo sapien
3	523	68.7	117	1 KVIJ HUMAN	P01601 homo sapien
4	508	66.8	129	1 KVIJ HUMAN	P04432 homo sapien
5	484	63.6	108	1 KVIJ HUMAN	P01611 homo sapien
6	478	62.8	128	1 KVS5 MOUSE	P01637 mus musculu
7	472.5	62.1	107	1 KVIJ HUMAN	P01596 homo sapien
8	472	62.0	108	1 KVIJ HUMAN	P01600 homo sapien
9	471	61.9	108	1 KVIJ HUMAN	P04430 homo sapien
10	470	61.8	108	1 KVIJ HUMAN	P01604 homo sapien
11	464	61.0	108	1 KVIJ HUMAN	P01598 homo sapien
12	464	61.0	108	1 KVIJ HUMAN	P01607 homo sapien
13	463	60.8	108	1 KVIJ HUMAN	P01610 homo sapien
14	462	60.7	108	1 KVIJ HUMAN	P01599 homo sapien
15	458	60.2	108	1 KVIJ HUMAN	P01594 homo sapien
16	457	60.1	108	1 KVIJ HUMAN	P01606 homo sapien
17	453.5	59.6	129	1 KVIJ HUMAN	P18136 homo sapien
18	452.5	59.5	129	1 KVIJ HUMAN	P18135 homo sapien

19	451	59.3	108	1 KVIJ HUMAN	P01597 homo sapien
20	451	59.3	108	1 KVIJ HUMAN	P01605 homo sapien
21	450	59.1	108	1 KVIJ HUMAN	P01608 homo sapien
22	445	58.5	108	1 KVIJ HUMAN	P01595 homo sapien
23	445	58.5	108	1 KVIJ HUMAN	P03662 homo sapien
24	442.5	58.1	129	1 KVIJ HUMAN	P04207 homo sapien
25	442	58.1	108	1 KVIJ HUMAN	P01593 homo sapien
26	441	58.0	108	1 KVIJ HUMAN	P01603 homo sapien
27	437	57.4	130	1 KVS5 MOUSE	P01639 mus musculu
28	435	57.2	128	1 KVIJ HUMAN	P06311 homo sapien
29	432	56.8	108	1 KVIJ HUMAN	P01609 homo sapien
30	430	56.5	115	1 KVSF MOUSE	P01608 mus musculu
31	422	55.5	134	1 KVIJ HUMAN	P06314 homo sapien
32	414	54.4	115	1 KVIJ HUMAN	P04433 homo sapien
33	413.5	54.3	109	1 KVIJ HUMAN	P01612 homo sapien
34	410	53.9	108	1 KVS5 MOUSE	P01644 mus musculu
35	407	53.5	132	1 KVIJ HUMAN	P01658 mus musculu
36	406	53.4	131	1 KVIJ HUMAN	P01661 mus musculu
37	405	53.2	108	1 KVS5 MOUSE	P01645 mus musculu
38	405	53.2	108	1 KVS5 MOUSE	P01648 mus musculu
39	405	53.2	108	1 KVS5 MOUSE	P01649 mus musculu
40	404.5	53.2	133	1 KVIJ HUMAN	P06313 homo sapien
41	404	53.1	115	1 KVS5 MOUSE	P01635 mus musculu
42	402	52.8	108	1 KVS5 MOUSE	P01636 mus musculu
43	401.5	52.8	116	1 KVIJ HUMAN	P04434 homo sapien
44	400	52.6	108	1 KVS5 MOUSE	P01646 mus musculu
45	398.5	52.4	109	1 KVIJ HUMAN	P01622 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	KVIW HUMAN	STANDARD;	PRT;	129 AA.
AC	P04431			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DE	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Walker precursor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014148; PubMed=6091049;			
RA	Klobeck H.G., Combrato G., Zachau H.G.;			
RT	"Immunoglobulin genes of the kappa light chain type from two human			
RT	lymphoid cell lines are closely related.";			
RL	Nucleic Acids Res. 12:6995-7006(1984).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X00965; CAA25477.1; ALT_TERM.			
DR	PIR; A01883; KIHUWK.			
DR	HSSP; P01607; 1REI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	Immunoglobulin V region; Signal.			
KW	SIGNAL	1	22	
FT	CHAIN	23	129	IG KAPPA CHAIN V-I REGION WALKER.
FT	DOMAIN	23	45	FRAMEWORK-1.
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	57	71	FRAMEWORK-2.
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-2.

DR	EMBL; J00245; AAS59087.1; -	FT	SIGNAL	1	22	IG KAPPA CHAIN V-I REGION HK102.
DR	EMBL; Z00001; CAA77292.1; -	FT	CHAIN	23	>117	FRAMEWORK-1.
DR	PIR; A01982; KIHU12.	FT	DOMAIN	23	45	COMPLEMENTARITY-DETERMINING-1.
DR	HSSP; P01607; 1REI.	FT	DOMAIN	46	56	FRAMEWORK-2.
DR	Genew; HGNC:5741; IGKV1-5.	FT	DOMAIN	57	71	COMPLEMENTARITY-DETERMINING-2.
DR	InterPro; IPR003006; IG_MHC.	FT	DOMAIN	72	78	FRAMEWORK-3.
DR	InterPro; IPR003596; IG_V.	FT	DOMAIN	79	110	COMPLEMENTARITY-DETERMINING-3.
DR	Pfam; PF00047; Ig; 1.	FT	DOMAIN	111	>117	BY SIMILARITY.
DR	SMART; SM00406; IGV; 1.	FT	DISULFID	45	110	
KW	Immunoglobulin V region; Signal.	FT	NON_TER	117	117	
FT	SIGNAL	FT	SEQUENCE	117 AA; 12768 MW; ADLDF3A40AFIA49B	CRC64;	
Alignment Scores:						
Pred. No.:	6.58e-48	Length:	117			
Score:	531.00	Matches:	100			
Percent Similarity:	94.74%	Conservative:	8			
Best Local Similarity:	87.72%	Mismatches:	6			
Query Match:	69.78%	Indels:	0			
DB:	1	Gaps:	0			
US-08-728-463B-220 (1-420) x KVIJ_HUMAN (1-117)						
QY	13 ATGATGTCGCCAGTCACGTCCTCGGTCTCTGCTGCTGCTTCCAGGTTCCAGATGC	132				
Db	3 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuProGlyAlaLysCys	22				
QY	73 GACATCCAGATGACCCAGTCCTCCATCTTCCGCTGTCATCTGTAGGAGACAGAGTCACC	132				
Db	23 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr	42				
QY	133 ATCACTTCGCGGAGTCAGATATTAGCAGCTGGTAGCTGGATCATCAGCATAACCA	192				
Db	43 IleThrCysArgAlaSerGlnSerIleSerSerTrpLeuAlaTrpTrpGlnGlnLysPro	62				
QY	193 GGTAAGCACCTAAAGCTCCTGATCTATGCTGCATCCAGTTTGAAAGTGGTGTCCCATCA	252				
Db	63 GlyLysAlaProLysLeuLeuIleTyrAspAlaSerSerLeuGluSerGlyValProSer	82				
QY	253 AGGTTACGGGAAGTGATCTGGAGACAGATTCTACTCTACCATCAGCAGCCTGCACGCT	312				
Db	83 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro	102				
QY	313 GAAGATTTTGCACCTACTATTGTCAACAGCCTAATAGTTTC	354				
Db	103 AspAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSerTyr	116				
RESULT 3.						
ID	KVII HUMAN	STANDARD;	PRT;	117 AA.		
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Ig kappa chain V-I region HK101 precursor (Fragment)					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
NCBI	TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=8109866; PubMed=6779204;					
RT	Bentley D.L., Rabbitts T.H.;					
RT	Human immunoglobulin variable region genes -- DNA sequences of two V					



QY 193 GGTAAAGCACCTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGTGTCCTCCATCA 252  
 DB 63 GlyLysAlaProThrLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyValProSer 82  
 QY 253 AGTTTCAGCGAAGTGGATCTGGACAGATTCTCTCCACCATCAGACGCTCGACGCT 312  
 DB 83 ArgPheSerGlySerGlyAlaGluPheThrLeuThrIleSerSerLeuGlnPro 102  
 QY 313 GAAGATTTCGAATCTACTATTGTCACAGAGCTAATGTTCCGTCACACTTTGGTCAG 372  
 DB 103 GluAspPheAlaThrTyrTyrCysGlnGlnAsnTyrAsnPheSerPheThrPheGlyGly 122  
 QY 373 GGAACCAAGCTGGAGATCAAA 393  
 DB 123 GlyThrLysValAspAsnLys 129

## RESULT 5

KV1S HUMAN STANDARD; PRT; 108 AA.  
 AC P01611;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Wes.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81092279; PubMed=6778806;  
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolysate of a protein by  
 RT high-pressure liquid chromatography. The primary structure of a  
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein  
 RT Wes).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

PIR; A01877; KIHUMS.  
 DR HSP; P80362; LWTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

## Alignment Scores:

Pred. No.: 5,6e-43 Length: 108  
 Score: 484.00 Matches: 93  
 Percent Similarity: 93.52% Conservative: 7  
 Best Local Similarity: 86.11% Mismatches: 0  
 Query Match: 63.60% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x KV1S\_HUMAN (1-108)

QY 73 GACATCAGATGACCCAGTCTCCATCTCCGTGTCATCTGTAGGAGACAGAGTCACC 132  
 DB 1 AspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAspArgValThr 20  
 QY 133 ATCACTTGTCGGGCGAGTACAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 192

DB 21 IleThrCysArgAlaSerGlnAspIleSerHisTyrLeuAlaTyrGlnGlnLysSer 40  
 QY 193 GGTAAAGCACCTAAGCTCTGATCTATGCTGATCCAGTTTGCAGAGTGGTGTCCTCCATCA 252  
 DB 41 GlyLysAlaProThrLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyValProSer 60  
 QY 253 AGTTTCAGCGAAGTGGATCTGGACAGATTCTCTCCACCATCAGACGCTCGACGCT 312  
 DB 61 ArgPheSerGlySerGlyAlaGluPheThrLeuThrIleSerSerLeuGlnPro 80  
 QY 313 GAAGATTTCGAATCTACTATTGTCACAGAGCTAATGTTCCGTCACACTTTGGTCAG 372  
 DB 81 GluAspPheAlaThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100  
 QY 373 GGAACCAAGCTGGAGATCAAA 396  
 DB 101 GlyThrThrValAspIleLysArg 108

## RESULT 6

KV5E MOUSE STANDARD; PRT; 128 AA.  
 AC P01637;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-V region T1 precursor.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81052342; PubMed=6776411;  
 RA Altenburger W., Steinmetz M., Zachau H.G.;  
 RT "Functional and non-functional joining in immunoglobulin light chain  
 RT genes of a mouse myeloma.";  
 RL Nature 287:603-607(1980).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).

EMBL; V00772; CAA24150.1; -  
 DR PIR; A01920; KVMST1.  
 DR HSP; P80362; LWTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 69 FRAMEWORK-2.  
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 77 108 FRAMEWORK-3.  
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 118 127 FRAMEWORK-4.  
 FT DISULFID 43 108 BY SIMILARITY.  
 FT NON\_TER 128 128  
 SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

## Alignment Scores:

Pred. No.: 2,44e-42 Length: 128  
 Score: 478.00 Matches: 88  
 Percent Similarity: 82.81% Conservative: 18  
 Best Local Similarity: 66.75% Mismatches: 22



US-08-728-463B-220 (1-420) x KVID\_HUMAN (1-107)

QY	73	GACATCCAGATGACCCAGCTCCATCTTCCTGCTGTCATCTGTAGGAGACAGAGTCACC	133
Db	1	AspIleGlnMeThrGlnSerProSerThrLeuSerAlaSerValGlyAspGVala	20
QY	133	ATCACTTGTGCGGCGAGTCAGGATATAGCAGCTGGTGTAGCCTGGTATCAGCATAAACCA	192
Db	21	IleThrCysArgAlaSerGlnAsnIleSerSerTrpLeuAlaTPTyTGlnGlnLysPro	40
QY	193	GGTAAGACACCTAAGCTCCTGATCTATCTGCTGCATCCAGCTTTGCAAGATGGTGTCCTCA	252
Db	41	GlyLysAlaProLysValLeuIleTyrLysSerSerLeuGluSerGlyValProSer	60
QY	253	AGGTTTCAGCGGAAGGAGTCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAGCCCT	312
Db	61	ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu***Pro	80
QY	313	GAAGATTTTGCACACTTACTATTGTCAACAGAGCTAATAGTATTCCTGCTACACTTTTGGT	372
Db	81	*****PheAlaThrTyrTyCysGlnGlnTyrAsnThrPhe---PheThrPheGlyPro	99
QY	373	GGAACCAAGCTGGAGATCAACAGCA	396
Db	100	GlyThrLysValAspIleLysArg	107

RESULT 8

KVID_HUMAN			
ID	KVID_HUMAN	STANDARD;	PRT; 108 AA.
AC	P01600;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-I region Hau.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI	TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=71032830; PubMed=4097974;		
RA	Watanabe S., Hilschmann N.;		
RT	"The primary structure of a monoclonal kappa-type immunoglobulin L-		
RT	chain of subgroup I (Bence-Jones Protein Hau): subdivision within		
RT	subgroups. I.		
RL	Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).		
CC	-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.		
CC	-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.		
DR	PIR; A01868; K1HUHU.		
DR	HSSP; P80362; 1WTL.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
KW	Immunoglobulin V region; Bence-Jones protein.		
FT	DOMAIN 1 23		
FT	DOMAIN 24 34		
FT	DOMAIN 35 49		
FT	DOMAIN 50 56		
FT	DOMAIN 57 88		
FT	DOMAIN 89 97		
FT	DOMAIN 98 107		
FT	DISULFID 23 88		
FT	NON_TER 108 108		
SQ	SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;		

Alignment Scores:

Pred. No.:	1,02e-41	Length:	108
Score:	472.00	Matches:	92
Percent Similarity:	92.59%	Conservative:	8
Best Local Similarity:	85.19%	Mismatches:	8
Query Match:	62.02%	Indels:	0

DB: 1 1 Gaps: 0

US-08-728-463B-220 (1-420) x KV1V\_HUMAN (1-108)

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGATCTGTAGGACAGAGTCACC 132  
 |||||  
 Db 1 AspileGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 |||||  
 QY 133 ATCAGTTGTGGCGGAGTCCAGATATTAGCAGCTGGTGTAGCTGATCAGCATAAACCA 192  
 |||||  
 Db 21 IleThrCysArgAlaSerGlnSerIleSerSerTyLeuSerTrpTyrGlnGlnLysPro 40  
 |||||  
 QY 193 GGTAAAGCACCTAAGCTCTGATCTATGCTGATCCAGTTTCGAAAGTGGTGTCCCATCA 252  
 |||||  
 Db 41 GlyLysAlaProGlnValLeuIleTyrAlaAlaSerSerLeuProSerGlyValProSer 60  
 |||||  
 QY 253 AGTTTCAGGGGAGTGGATCTGGGACAGATTTCACTCTCACATCAGCAGCTCGAGCCT 312  
 |||||  
 Db 61 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80  
 |||||  
 QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372  
 |||||  
 Db 81 GluAspPheAlaThrTy-TyrCysGlnGlnAsnTyrIleThrProThrSerPheGlyGln 100  
 |||||  
 QY 373 GGAACCAAGCTGGAGATCAACAGCA 396  
 |||||  
 Db 101 GlyThrArgValGluIleLysArg 108

RESULT 9

KV1V\_HUMAN STANDARD; PRT; 108 AA.

AC P04430;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region BAN.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86174817; PubMed=3083240;  
 RA Dulet F.E., O'Connor T.P., Benson M.D.;  
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";  
 RL Mol. Immunol. 23:73-78 (1986).  
 DR PIR; A01878; KIHUBN.  
 DR HSSP; P80362; 1WTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 KW Immunoglobulin V region; Amyloid.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Alignment Scores:

Pred. No.: 1.3e-41 Length: 108  
 Score: 471.00 Matches: 88  
 Percent Similarity: 92.59% Conservative: 12  
 Best Local Similarity: 81.48% Mismatches: 8  
 Query Match: 61.89% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x KV1V\_HUMAN (1-108)

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGGTGTCTGATCTGTAGGACAGAGTCACC 132  
 |||||  
 Db 1 AspileGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20  
 |||||  
 QY 133 ATCAGTTGTGGCGGAGTCCAGATATTAGCAGCTGGTGTAGCTGATCAGCATAAACCA 192  
 |||||  
 Db 21 IleThrCysArgAlaSerGlnSerValTyrAsnTyrValAlaTrpPheGlnGlnLysPro 40  
 |||||  
 QY 193 GGTAAAGCACCTAAGCTCTGATCTATGCTGATCCAGTTTCGAAAGTGGTGTCCCATCA 252  
 |||||  
 Db 41 GlyLysAlaProLysSerLeuIleTyrAspAlaSerThrLeuGlnSerGlyValProSer 60  
 |||||  
 QY 253 AGTTTCAGGGGAGTGGATCTGGGACAGATTTCACTCTCACATCAGCAGCTCGAGCCT 312  
 |||||  
 Db 61 AsnPheThrGlySerGlySerGlyThrAspPheIleLeuThrIleSerSerLeuGlnPro 80  
 |||||  
 QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372  
 |||||  
 Db 81 GluAspPheAlaThrTy-TyrCysGlnGlnTyrAsnSerTyrProTyrThrPheGlyGln 100  
 |||||  
 QY 373 GGAACCAAGCTGGAGATCAACAGCA 396  
 |||||  
 Db 101 GlyThrLysValGlnIleLysArg 108

RESULT 10

KV1L\_HUMAN STANDARD; PRT; 108 AA.

AC P01604;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Kue.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79237924; PubMed=112021;  
 RA Eulitz W., Kley H.-P., Zeitler H.-J.;  
 RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
 sequence of the variable part of a human L-chain of the kappa-type.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734 (1979).  
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR PIR; A01870; KIHUKU.  
 DR HSSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGv; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Alignment Scores:

Pred. No.: 1.65e-41 Length: 108  
 Score: 470.00 Matches: 88  
 Percent Similarity: 91.67% Conservative: 11  
 Best Local Similarity: 81.48% Mismatches: 9  
 Query Match: 61.76% Indels: 0  
 DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x KV1L\_HUMAN (1-108)

```
QY 73 GACATCCAGTACCAGTCTCCATCTTCGGTCTGTCATCTGTAGGACAGAGTCACC 132
Db 1 AspileGlnMetThrGlnSerProSerThrGlnProAlaSerValGlyAspArgValThr 20
QY 133 ATCACTTGTCCGGCGAGTACAGATATTAGCAGCTGGTGTAGCCCTGATCAGCATAAACCA 192
Db 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrLeuAlaThrPyrGlnGlnLysPro 40
QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGTGTCCCATCA 252
Db 41 GluLysAlaProLysLeuLeuIleThrLysAlaSerThrLeuGluThrGlyValProSer 60
QY 253 AGCTTCAGCGAGTGGATCGGACAGATTTCACTCTCACCATCAGCAGCCCTGCAGCCT 312
Db 61 ArgPheSerGlySerGlyThrGluPheThrLeuThrIleAsnSerLeuGlnPro 80
QY 313 GAAGATTTTGCACCTTACTATTCTCAACAGGCTTAAGTTTCCCGTACACTTTTGTGTG 372
Db 81 AspAspPheAlaThrTyThrCysGlnGlnTyThrSerArgTyThrPheGlyGln 100
QY 373 GGAACCAAGCTGGAGATCAACGA 396
Db 101 GlyThrLysLeuAspileLysArg 108
```

## RESULT 11

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KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=71064023; PubMed=5489770;
RX Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01866; KIHUEU.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
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## Alignment Scores:

Pred. No.: 7.05e-41 Length: 108

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Score: 464.00 Matches: 88
Percent Similarity: 91.59% Conservative: 10
Best Local Similarity: 82.24% Mismatches: 9
Query Match: 60.97% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x KVIF_HUMAN (1-108)

QY 73 GACATCCAGTACCAGTCTCCATCTTCGGTCTGTCATCTGTAGGACAGAGTCACC 132
Db 1 AspileGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 20
QY 133 ATCACTTGTCCGGCGAGTACAGATATTAGCAGCTGGTGTAGCCCTGATCAGCATAAACCA 192
Db 21 IleThrCysArgAlaSerGlnSerIleAsnIleThrLeuAlaThrPyrGlnGlnLysPro 40
QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGTGTCCCATCA 252
Db 41 GlyLysAlaProLysLeuLeuMetTyThrLysAlaSerSerLeuGluSerGlyValProSer 60
QY 253 AGCTTCAGCGAGTGGATCTCGGACAGATTTCACTCTCACCATCAGCAGCCCTGCAGCCT 312
Db 61 ArgPheIleGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80
QY 313 GAAGATTTTGCACCTTACTATTCTCAACAGGCTTAAGTTTCCCGTACACTTTTGTGTG 372
Db 81 AspAspPheAlaThrTyThrCysGlnGlnTyThrAsnSerAspSerLysMetPheGlyGln 100
QY 373 GGAACCAAGCTGGAGATCAACGA 393
Db 101 GlyThrLysValGluValLys 107

RESULT 12
KVIF_HUMAN
ID KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT FRAMEWORK-1.
```



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059122; PubMed=4215718;  
 RA Laure C.J., Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 (macroglobulin Gal.), I. The amino acid sequence of the L-chain of  
 RT kappa-type, subgroup I.";  
 RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504 (1973).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN.  
 DR PIR; A01867; KIHUGL.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; CIAD3CB0F600FF73 CRC64;  
 Alignment Scores:  
 Pred. No.: 1,14e-40 Length: 108  
 Score: 462.00 Matches: 90  
 Percent Similarity: 90.74% Conservative: 8  
 Best Local Similarity: 83.33% Mismatches: 10  
 Query Match: 60.71% Indels: 0  
 DB: 1 Gaps: 0  
 US-08-728-463b-220 (1-420) x KV1G\_HUMAN (1-108)  
 QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGTCATCTGTAGGAGACAGATCACC 132  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 133 ATCACTTGTCGGCGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATAAACCA 192  
 Db 21 IleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuThrTrpTyrGlnGlnLysPro 40  
 QY 193 GGTAAAGACCACTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAGAGTGGTGTCCCATCA 252  
 Db 41 GlyLysAlaProLysGlnLeuLeuIleTyrAlaAlaSerAsnLeuGlnSerGlyValProSer 60  
 QY 253 AGTTTCAGCGAAGTGGATCTGGACAGATTTCACTCTACCATCAGACGCTGCAGCCT 312  
 Db 61 ArgPheSerGlySerGlyAlaGlyThrGluPheThrLeuThrIleSerSerLeuGlnPro 80  
 QY 313 GAAGATTTTGCACCTTACTTCTCAACAGGCTAATAGTTTCCGTCACATTTTGTGTGTCAG 372  
 Db 81 GluAspPheAlaThrTyrTyrCysLeuGlnGlnAsnSerTyrProArgSerPheGlyGln 100  
 QY 373 GGAACCAAGCTGGAGATCAACCA 396  
 Db 101 GlyThrLysValGluLeuLysArg 108  
 RESULT 15  
 KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein Au).";  
 RL Hoppe-Sevler's Z. Physiol. Chem. 353:345-370 (1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RT Bence-Jones protein Au.";  
 RL Biophys. Struct. Mech. 1:139-146 (1975).  
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REI.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; E8011187B56F6B9 CRC64;  
 Alignment Scores:  
 Pred. No.: 3.01e-40 Length: 108  
 Score: 458.00 Matches: 88  
 Percent Similarity: 88.89% Conservative: 8  
 Best Local Similarity: 81.48% Mismatches: 12  
 Query Match: 60.18% Indels: 0  
 DB: 1 Gaps: 0  
 US-08-728-463b-220 (1-420) x KV1B\_HUMAN (1-108)  
 QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGTCATCTGTAGGAGACAGATCACC 132  
 Db 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
 QY 133 ATCACTTGTCGGCGAGTCAGGATATTAGCAGCTGGTGTAGCCTGGTATCAGCATAAACCA 192  
 Db 21 IleThrCysGlnAlaSerGlnAspIleSerAspTyrLeuAsnTrpTyrGlnGlnLysPro 40  
 QY 193 GGTAAAGACCACTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAGAGTGGTGTCCCATCA 252  
 Db 41 GlyLysAlaProLysLeuLeuIleTyrAspAlaSerAsnLeuGlnSerGlyValProSer 60  
 QY 253 AGTTTCAGCGAAGTGGATCTGGACAGATTTCACTCTACCATCAGACGCTGCAGCCT 312  
 Db 61 ArgPheSerGlySerGlyAlaHisPheThrPheThrIleSerSerLeuGlnPro 80  
 QY 313 GAAGATTTTGCACCTTACTTCTCAACAGGCTAATAGTTTCCGTCACATTTTGTGTGTCAG 372  
 Db 313 GAAGATTTTGCACCTTACTTCTCAACAGGCTAATAGTTTCCGTCACATTTTGTGTGTCAG 372

Db 81 GluAspIleAlaThrTyrTyrCysGlnGlnTyrAspTyrLeuProTyrThrPheGlyGln 100  
QY 373 GGAACCAAGCTGGAGATCAACGA 396  
Db 101 GlyThrLysValGluIleLysArg 108

Search completed: June 3, 2003, 09:04:11  
Job time : 9.96662 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 37.2838 Seconds  
(without alignments)  
4642.224 Million cell updates/sec

Title: US-08-728-463B-220  
Perfect score: 761  
Sequence: 1 AAGCTTGCCACCATGATGTT.....TGCTGCACCATCTGTCCTC 420

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/cgn2.1/USPTO.spool/US08728463/runat\_03062003\_085614\_16815/app\_query.fasta\_1.3690  
-DB=SPTRMBL 21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08728463 @CGN 1.1.380 @runat\_03062003\_085614\_16815 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phase: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	492	64.7	234	11	Q8R062 mus musculus

ID	Q8R062	PRELIMINARY;	PRT;	234 AA.
AC	Q8R062;			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Hypothetical 25.9 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=COLON;			
RA	Strausberg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC027418; AAH27418.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;			

Alignment Scores:  
Pred. No.: 7.64e-47 Length: 234  
Score: 492.00 Matches: 97  
Percent Similarity: 82.22% Conservative: 14





Qy	253	AGGTTTCAGCGGAAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGCTGCAGCCT	312
Db	81	ArgPheSerGlySerArgSerGlyThrGlnPheSerLeuLysIleAsnSerLeuGlnPro	100
Qy	313	GAGATTTTGCACCTTACTATTGTCAACAGCCTAATAGTTTCCCGTACACTTTTGGTTCAG	372
Db	101	GluAspPheGlySerTyrTyrrCysGlnHisSerGlyIleProPheThrPheGlySer	120
Qy	373	GGAAACCAAGCTGGAGATCAACGAACACTGTGGCTGCACCATCTGTC	417
Db	121	GlyThrLysLeuGluIleLysArgAlaAspAlaProThrVal	135

01-MAY-2000 (TRENBLREL. 13, Created)  
DT  
01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT  
01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
DE  
DE Myosin-reactive immunoglobulin light chain variable region  
DE (fragment).  
DE  
OS Homo sapiens (Human).  
OS  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC  
NCBI TaxID=9606;  
OX

KN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	

Young D.C.;  
"Myosin-reactive a

RT  
Pr  
tetug. " ;  
Clin. Tm

DR EMBL; AF035044; AAD56280.1; -.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; ig; 1.

FT	NON TER	1
FT	NON TER	1

FI	NON_IER	I08
SO	SEQUENCE	108 AA: 11633, MW

[illegible]

Pred. No.: 2.59e-45

Percent Similarity:	91.67%	Conservative:	5
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Query Match:	62.81%	Indels:	0
DB:	4	Gaps:	0
US-08-728-463B-220 (1-420) x Q9UL70 (1-108)			
QY	73	GACATCCAGATACCCAGATCTCCATCTCCGTGTCTGCATCTG	

Db  
1 Asn11eGlnMetThrGlnSerProSerSe

QY 133 ATCACTTGTGCGGGGAGTCAGGATATTAGCAGCTGTTAGCTGCTATCAGCATAAACCA 192

Db 21 IlethrCysArgAlaSerGlnGlyIleSerAsnTyrLeuAlaTrpTyrGlnGlnLysPro 40

Qy	193	GGTAAAGCACCTAAAGCTCCTGATCTATGTGTCATCCAGTTTTGCAAAAGTGGTGTCGCATCA
Db	41	GLYLYSVALPROLYSSERLEUILETYRALAALASERTHRLEUGINSERGLVALPROSER

Qy	253	AGTTTCACGGAGTGGATCTCTGGACAGATTTCATCTCTCA	CCATCAGCAGCGCTGCAGCCT	312
Dp	61	AtcPheSerGlvSerGlvSerGlvThrAspPheThrLeuThrIleSerSerLeuGlnPro		80

Qy	313	GAAGATTTTGC	AACCTTACTAT	TGTCACACAGG	CTAATAGTTTCC	CGTACACTTTT	GGTGCAG	372
Db	81	GluAspValAla	AlaThrTyrTyr	CysGlnLeuTyr	AsnSerAlaPro	ArgThrPheGly	Pro	100

QY 373 GGAACCAAGCTGGAGATCAACGA 396  
 DB 101 GlyThrLysLeuGlulileysArg 108

RESULT 6  
 Q96SA9 PRELIMINARY; PRT; 107 AA.  
 AC Q96SA9  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain.  
 DE variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98375893; PubMed=9712075;  
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
 RT "Molecular analysis of polyclonal antibodies from  
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
 RT antibody V region genes";  
 RL J. Immunol. 161:2020-2031(1998).  
 DR EMBL; U96396; AAB68785.1; -.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Alignment Scores:  
 Pred. No.: 4.96e-45 Length: 107  
 Score: 475.50 Matches: 96  
 Percent Similarity: 92.59% Conservative: 4  
 Best Local Similarity: 88.89% Mismatches: 7  
 Query Match: 62.48% Indels: 1  
 DB: 4 Gaps: 1

US-08-728-463B-220 (1-420) x Q96SA9 (1-107)

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGCTGCTGATCTGTAGGAGACAGATCACC 132  
 DB 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValGlyAspArgValThr 20

QY 133 ATCACTTGTGGCGAGTACAGATATTAGCAGCTGGTTCAGCTGATCAGCATAACCA 192  
 DB 21 IleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsnTrpTyrGlnGlnLysPro 40

QY 193 GGTAAAGCAGCTAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAGTGTGCCATCA 252  
 DB 41 GlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSer 60

QY 253 AGGTTACGCGAGTGGATCTGGACAGATTTCACTCTCACCATCAGCCCTGCAGCCT 312  
 DB 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 80

QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372  
 DB 81 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSer---ThrLeuThrPheGlyGly 99

QY 373 GGAACCAAGCTGGAGATCAACGA 396  
 DB 100 GlyThrLysValGlulileysArg 107

RESULT 7  
 Q9UL79 PRELIMINARY; PRT; 108 AA.  
 ID Q9UL79  
 AC Q9UL79  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035035; NAD56271.1; -.  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR NON\_TER 1 1  
 DR NON\_TER 108 108  
 FT NON\_TER 108 AA; 11787 MW; DB5845F19724FB4E CRC64;  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Alignment Scores:  
 Pred. No.: 2.16e-43 Length: 108  
 Score: 461.00 Matches: 91  
 Percent Similarity: 89.81% Conservative: 6  
 Best Local Similarity: 84.26% Mismatches: 11  
 Query Match: 60.58% Indels: 0  
 DB: 4 Gaps: 0

US-08-728-463B-220 (1-420) x Q9UL79 (1-108)

QY 73 GACATCCAGATGACCCAGTCTCCATCTTCGCTGCTGATCTGTAGGAGACAGATCACC 132  
 DB 1 AspIleValMetThrGlnSerProSerLeuSerAlaSerThrGlyAspArgValThr 20

QY 133 ATCACTTGTGGCGAGTACAGATATTAGCAGCTGGTTCAGCTGATCAGCATAACCA 192  
 DB 21 IleSerCysArgMetSerGlnGlyIleSerSerTyrLeuAlaTrpTyrGlnGlnLysPro 40

QY 193 GGTAAAGCAGCTTAACTCTGATCTATGCTGCATCCAGTTTGCAGAGTGTGCCATCA 252  
 DB 41 GlyLysAlaProGluLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSer 60

QY 253 AGGTTACGCGAGTGGATCTGGACAGATTTCACTCTCACCATCAGCCCTGCAGCCT 312  
 DB 61 ArgPheSerGlySerGlyThrAspPheThrLeuThrIleSerCysLeuGlnSer 80

QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAG 372  
 DB 81 GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerPheProThrPheGlyGln 100

QY 373 GGAACCAAGCTGGAGATCAACGA 396  
 DB 101 GlyThrLysValGlulileysArg 108

RESULT 8  
 Q96PF6 PRELIMINARY; PRT; 116 AA.  
 ID Q96PF6  
 AC Q96PF6  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
 DE Kappa 1 light chain variable region (Fragment).  
 DE SDNK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.

```

RX MEDLINE-21361171; PubMed-11468171;
RA Comenzó R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Alignment Scores:
Pred. No.: 6.18e-43 Length: 116
Score: 457.00 Matches: 87
Percent Similarity: 86.21% Conservative: 13
Best Local Similarity: 75.00% Mismatches: 16
Query Match: 60.05% Indels: 0
DB: 4 Gaps: 0

US-08-728-463B-220 (1-420) x Q96PF6 (1-116)
QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGTCATCTGTAGGACAGAGTCACC 132
Db 1 AspilleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20
QY 133 ATCACTTGTGGCGAGTCAGGATATTAGCAGTGTAGCTGTAGCTGGTATCAGCATAACCA 192
Db 21 PheileCysGlnAlaSerGlnAspIleAlaAsnHisLeuAsnTrpYrGlnLysLysPro 40
QY 193 GGTAAGACCTTAAGCTCTGATCTATGCTGATCGATCCAGTTTGCAGAGTGTGCCATCA 252
Db 41 GlyGluAlaProLysPheLeuIleTyAspGlySerPheLeuLysThrGlyValProSer 60
QY 253 AGCTTCAGCGGAGTGGATCTGGACAGATTCACATCTCCATCAGCAGCCCTGCAGCCT 312
Db 61 ArgPheSerGlyGlyGlySerAlaThrAsnPhenThrValThrIleSerSerLeuGlnPro 80
QY 313 GAAGATTTTGCACCTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGTGTCAG 372
Db 81 GluAspPheAlaThrTyTyCysGlnGlnTyHisLeuProPheThrPheGlyPro 100
QY 373 GGAAACAGCTGGAGATCAACAGCACTGTGGCTGCGACCATCTGCTCTTC 420
Db 101 GlyThrLysValAspPheLysArgThrValAlaAlaProSerValPhe 116

RESULT 9
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Alignment Scores:
Pred. No.: 3.31e-42 Length: 107
Score: 450.50 Matches: 90
Percent Similarity: 89.81% Conservative: 7
Best Local Similarity: 83.33% Mismatches: 10

```

```

Pred. No.: 1.95e-42 Length: 233
Score: 453.00 Matches: 89
Percent Similarity: 81.60% Conservative: 13
Best Local Similarity: 71.20% Mismatches: 23
Query Match: 59.53% Indels: 0
DB: 11 Gaps: 0

US-08-728-463B-220 (1-420) x Q91WS9 (1-233)
QY 43 CTGCTGCTCTGTTCCAGATGCGATCCAGATCCAGATCCAGTCTCCATCTTCC 102
Db 10 LeuLeuLeuCysPheGlnGlySerArgCysAspIleGlnMetThrGlnThrThrSerSer 29
QY 103 GTGCTGCTCTGTAGGACAGATCCATCATCTGTGCGGCGAGTCAGGATATTAGC 162
Db 30 LeuSerAlaSerLeuGlyAspArgValThrIleSerCysSerGlySerGlnGlyIleAla 49
QY 163 AGCTGTTAGCTGTATCAGCATTAACCCAGGTAAAGCACCTAAAGCTCTGATCTATGCT 222
Db 50 AsnTyLeuAsnTrpYrGlnGlnLysProAspGlyThrValLysLeuLeuIleTyTy 69
QY 223 GCATCCAGTTTCAAAAGTGGTCTCCATCAAGTTTCAGCGGAAGTGGATCTGGACAGAT 282
Db 70 ThrSerSerLeuHisSerGlyValProSerArgPheSerGlySerGlyThrAsp 89
QY 283 TTCATCTCACCATCAGCAGCTGCGCTGAGAGTTTTCGAATTTTGAATTTACTATTGTCACAG 342
Db 90 TyrSerLeuThrIleSerAsnLeuGluProGluAspIleAlaThrTyTyTyCysGlnGln 109
QY 343 GCTAATAGTTTCCGTACACTTTTGGTCAGGGAACCAAGCTGAGATCAACGAACTGTG 402
Db 110 TyrArgTyLeuProTrpThrPheGlyGlyThrLysLeuGluIleLysArgAlaAsp 129
QY 403 GCTGACCATCTGTC 417
Db 130 AlaAlaProThrVal 134

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; RAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Alignment Scores:
Pred. No.: 3.31e-42 Length: 107
Score: 450.50 Matches: 90
Percent Similarity: 89.81% Conservative: 7
Best Local Similarity: 83.33% Mismatches: 10

```





QY 298 AGCAGCTGCAGCCTGAAGATTGTCACCTACTATGTCACAGGCTAATAGTTCGCCG 357  
Db : : : : :  
101 ThrArgVal1Glu1aGluAerVal1GlyVal1PheCysMec1Ingl1yhrHstPro 120  
QY 358 TACACTTTGTGACGGGACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417  
Db : : : : :  
121 SerThrHeliGlnGln1yhrLysLeuGln1LeuVal1ArgVal1Ala1aProSerVal 140  
QY 418 TTC 420  
Db : : :  
141 Phe 141

## RESULT 13

Q9RIAS

ID Q9RIAS PRELIMINARY; PRT; 214 AA.

AC Q9RIAS; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Kappa light chain of Mab7 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wille K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;  
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
RT antibody (Mab 7, its light and heavy chains) and construction of a  
RT single chain antibody (scFv)."  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152371; AAD40242.1; -  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003600; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; IG\_1like; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
FT NON\_TER 1 1  
FT NON\_TER 214 214  
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

## Alignment Scores:

Pred. No.: 3,636-39 Length: 214  
Score: 424.00 Matches: 80  
Percent Similarity: 84.35% Conservative: 17  
Best Local Similarity: 69.57% Mismatches: 18  
Query Match: 55.72% Indels: 0  
DB: 11 Gaps: 0

US-08-728-463b-220 (1-420) x Q9RIAS (1-214)

QY 73 GACATCCAGATGACCCAGCTCTCATCTTCGTCGTCATCTGTAGAGACAGATCACC 132  
Db : : : : :  
1 Aspl1eGlnLeuThrGlnSerProSerSerMetCylAlaSerLeu1yGluAryVal1hr 20  
QY 133 ATCACTGTGGGGGAGATCAGATATTAAGAGCTGTGTAAGCTGTATCAGCAATAAACA 192  
Db : : : : :  
21 TleHrCylVal1aAlaSerGlnAser1LeuAser1yLeuSer1rPheGlnGln1ySerPro 40  
QY 193 GGTAAAGACCTAAGCTCTGATCTATGCTGATCAAGTTTGAAGTGTGTCCCATCA 252  
Db : : : : :  
41 G1yLysSerProLysThrLeu1le1y1rA1aAlaAser1yVal1aAlaProSer 60  
QY 253 AGCTTACGCGGAGATGATGTGGACAGATTTCACTTCACATCAGCAGCTGAGCCT 312  
Db : : : : :  
61 ArgPheSer1ySerGlySerGlyGlnAser1yLeu1rH1eSerSerLeuGln1y 80  
QY 313 GAAGATTTTGCACCTACTATGTCACAGGCTAATAGTTCCCGTACCTTTGGTCAG 372  
Db : : : : :  
81 GluAserMec1y1le1y1r1yCylVal1eGln1y1rAserGln1yPheProPheThrPheGlySer 100

QY 373 GGAACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417  
Db : : : : :  
101 GlyThrLysLeuGln1le1y1rA1aAlaAser1yVal1aAlaProThrVal 115

## RESULT 14

Q9QYF0

ID Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CN 8 scFv.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/C; TISSUE=SPLEEN;  
RX MEDLINE=20183931; PubMed=10706631;  
RA Shinohara N., Demura T., Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phage display subtraction  
RT method".  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).  
DR EMBL; AB036341; BAAB8633.1; -  
DR HSSP; P01607; 1REI.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

## Alignment Scores:

Pred. No.: 96-37 Length: 298  
Score: 403.00 Matches: 77  
Percent Similarity: 78.99% Conservative: 17  
Best Local Similarity: 64.71% Mismatches: 25  
Query Match: 52.96% Indels: 0  
DB: 11 Gaps: 0

US-08-728-463b-220 (1-420) x Q9QYF0 (1-298)

QY 61 GGTTCAGATGACCATCAGATGACCCAGCTCTCATCTTCGTCGATCTGTAGGA 120  
Db : : : : :  
169 Gly1yGlySerApl1eGlnLeuThrGlnSerPro1aSerLeuSerA1aSerVal1Gly 188  
QY 121 GACAGAGTCAACATCACTTGTGGGCGAGTCAGATATTAAGCACTGTGTAAGCTGTAT 180  
Db : : : : :  
189 GluThrVal1Thr1le1yHrCylAryAlaSer1yAser1yLeuA1a1rPlyr 208  
QY 181 CAGCTAAACAGGTAAGCACTTACCTCTGATCTATGCTGATCAGATTTGCAAGT 240  
Db : : : : :  
209 GlnGln1ySerGln1ySerProGlnLeuVal1yHrAser1yThrLeuA1a1rPlyr 228  
QY 241 GGTGCCATCAAGGTCAGCGGAGATGATCTGGGACAGATTTCACTTCACCATCAGC 300  
Db : : : : :  
229 GlyVal1ProSerA1aPheSerGlySerGlySer1yThrGln1ySerLeu1y1leAser 248  
QY 301 AGCTGAGCCTGAAGATTTTGAACCTTATGTTGAACAGGCTAATAGTTCCCGTAC 360  
Db : : : : :  
249 SerLeuGlnProGlnAserPheGlySer1y1yCylGln1h1shPheThrP1hrPro1y 268  
QY 361 ACTTTGTGAGGAACCAAGCTGAGATCAACAGCACTGTGCTGACCATCTGTC 417  
Db : : : : :  
269 ThrPhe1yGlyGln1yThr1yLeuGln1le1yAryAla1a1a1y1aProVal 287

## RESULT 15

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:21 ; Search time 27.1662 Seconds  
(without alignments)  
4120.219 Million cell updates/sec

Title: US-08-728-463B-220

Perfect score: 761  
Sequence: 1 AACCTGCCACCATGATGCT.....TGGCTGCACCATCTGCTTC 420

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 908470 segs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xid  
-O=cpm2.1/USPTO.spool/US08728463.r/unat.03062003.085613.16797/app.query.fasta.1.3690  
-DB=A.GeneSeq.101002 -QWMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US08728463 @CCN 1.1 353 @runat.03062003.085613.16797 -NCPU=6 -ICPU=3  
-NO MAMP -LARGEJOINT -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAFN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
A: GeneSeq.101002: \*  
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6: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT: \*  
7: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT: \*  
8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT: \*  
9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT: \*  
10: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT: \*  
11: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT: \*  
12: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT: \*  
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14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT: \*  
15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT: \*  
16: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT: \*  
17: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT: \*  
18: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT: \*  
19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT: \*  
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23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	656	86.2	236	23	AAU74297	Anti-human ALIIM m
2	621.5	81.7	241	22	AB82312	Human immune respo
3	610.5	80.2	234	14	AA38162	Sequence of the Ka
4	610.5	80.2	237	21	AA96298	Human IGFBP-10 imm
5	606.5	79.7	237	21	AA96289	Human IGFBP-1 immu
6	606.5	79.7	237	21	AA96301	Human IGFBP-13 imm
7	602	79.1	139	23	ABP43157	Human ovarian anti
8	601	79.0	260	23	ABP41164	Human ovarian anti
9	599	78.7	234	13	AA20058	Light chain of 3D6
10	597	78.4	146	22	AA899115	Human protein SEQ
11	591	77.7	234	18	AAW11638	Human anti-RSV mon
12	588	77.3	236	21	AA96297	Human anti-RSV mon
13	585.5	76.9	237	21	AB15546	Human immune syste
14	585	76.9	236	14	AA42065	Human anti-HBs 11g
15	582	76.5	130	16	AA75394	Anti-interleukin-1
16	578	76.0	128	17	AAW01527	Monoclonal antibod
17	578	76.0	128	18	AAW24990	Monoclonal antibod
18	578	76.0	130	21	AA56737	Amino acid sequenc
19	577	75.8	236	21	AA96293	Human IGFBP-5 immu
20	574	75.4	132	18	AAW2842	Human anti-tumour
21	568	74.6	124	21	AA56723	Amino acid sequenc
22	567	74.5	236	16	AA77614	Humanised 5G1.1 VL
23	567	74.5	236	23	ABP51696	5G1.1 light chain
24	565	74.2	134	23	AAW47645	Human protein sequ
25	564	74.1	129	19	AAW70379	Anti-human CD23 5E
26	562	73.9	129	21	AA56722	Amino acid sequenc
27	561	73.7	124	18	AAW10233	TF8-5G9 CDR-graft
28	560	73.6	129	23	ABG53326	Thrombopoietin ago
29	558.5	73.4	235	18	AAW11640	Human anti-RSV mon
30	557	73.2	129	16	AA65018	93K99 anti-Varicel
31	557	73.2	133	17	AA87057	CDR grafted anti-1
32	550	72.3	233	21	AA803713	Immunoglobulin kap
33	546	71.7	129	15	AA857482	Humanised 1308F VL
34	546	71.7	129	17	AA892085	Humanised antibody
35	543.5	71.4	128	21	AA56717	Amino acid sequenc
36	543	71.4	234	12	AA13050	CD4-specific CDR-g
37	543	71.4	238	21	AAW90330	Humanised anti-Fas
38	543	71.4	238	23	ABP74899	Humanised anti-Fas
39	542	71.2	129	21	AA56724	Amino acid sequenc
40	542	71.2	238	21	AA890932	Novel human diagno
41	542	71.2	238	21	AA890932	Humanised anti-Fas
42	542	71.2	238	23	ABP74901	Humanised anti-Fas
43	541	71.1	235	21	AA803684	Immunoglobulin kap
44	539	70.8	128	15	AA854053	Sequence of the VL
45	539	70.8	238	21	AAW90931	Humanised anti-Fas

## ALIGNMENTS

RESULT 1  
AAU74297  
AAU74297 standard; Protein; 236 AA.

AC AAU74297;  
XX 12-MAR-2002 (first entry)

DE Anti-human ALIIM monoclonal antibody clone Unab-136, light chain.

KW Human, antineumatic; antiarthritic; antiabiotic; antipsoriatic;  
KW antiallergic; antitumor; neuroprotective; antithyroid; vasotrophic;  
KW immunosuppressive; dermatological; antiinflammatory; hepatotropic;  
KW activation inducible lymphocyte immunomodulatory molecule; ALIIM;  
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;  
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;  
KW systemic lupus erythematosus; autoimmune disorder; inflammation;  
KW graft versus host reaction; immune rejection; intestinal immunity;

KM ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200187981-A2.  
 XX  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 15-MAY-2001; 2001MO-JP04035.  
 XX  
 PR 18-MAY-2000; 2000JP-0147116.  
 XX 30-MAR-2001; 2001JP-0099508.  
 XX  
 PA (NIBS) JAPAN TOBACCO INC.  
 XX  
 PI Teuji T, Tezuka K, Hori N;  
 XX  
 DR WPI; 2002-075313/10.  
 DR N-PSDB; AAS99473.  
 XX  
 PS Claim 30; Page 270-271; 300pp; English.  
 XX  
 PT New human monoclonal antibody that binds to activation inducible  
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid  
 PT arthritis, multiple sclerosis and inflammation  
 XX  
 XX

The invention relates to a novel human antibody (i), preferably a human  
 monoclonal antibody which binds to an activation inducible lymphocyte  
 immunomodulatory molecule (AILM). (i) is useful for modulating signal  
 transduction into a cell mediated by AILM, for modulating proliferation  
 of AILM-expressing cells, for inducing production of a cytokine from  
 AILM-expressing cells, and for inducing antibody-dependent cytotoxicity  
 against AILM-expressing cells and/or immune cytotoxicity or apoptosis of  
 AILM-expressing cells. (i) is useful for treating, preventing or  
 prophylaxis of delayed type allergy. (i) is useful for treating and  
 preventing various diseases associated with AILM-mediated  
 costimulatory transduction, and for inhibiting the onset and/or  
 advancement of the diseases. (i) is useful for suppression,  
 prevention and/or treatment of rheumatoid arthritis, multiple  
 sclerosis, autoimmune thyroiditis, allergic contact dermatitis,  
 chronic inflammatory dermatosis, systemic lupus erythematosus,  
 insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic  
 disorders, inflammation, graft versus host reaction, graft versus host  
 disease, immune rejection, disorders caused by abnormal intestinal  
 immunity, specifically inflammatory intestinal disorders such as  
 ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and  
 pancreatitis. (i) induces no serious immunorejection due to antigenicity  
 to human, i.e., human anti-mouse immunorejection (HAMA) in a host.  
 CC AAU74296-AAU74301 represent anti-human AILM monoclonal antibody amino  
 CC acid sequences of the invention.  
 CC  
 XX

Sequence 236 AA;

Alignment Scores:

Pred. No.: 1,066-61 Length: 236  
 Score: 656.00 Matches: 128  
 Percent Similarity: 95.59% Conservative: 2  
 Best Local Similarity: 94.12% Mismatches: 6  
 Query Match: 86.20% Indels: 0  
 DB: 23 Gaps: 0

US-08-728-463B-220 (1-420) x AAU74297 (1-236)

QY 13 ATGATGTCCTCCAGCTCAGCTCTCGGTCTCTGCTGTTCCAGGTTCCAGATGC 72  
 DB 3 MetArgValProIaGlnLeuLeuGlyLeuLeuLeuLeuTrpPheProGlySerArgCys 22  
 QY 73 GACATCCAGATGACCCAGCTCCATCTTCGTCGTCGTCATCTGTAGAGACAGATCACC 132  
 DB 23 AspIleIleMetTrpGlnSerProSerValSerValaSerValGlyAspArgValThr 42  
 QY 133 ATCATCTTGCGGGGAGTCAAGATATTAGCAGCTGTGTTACCTGTATCGATTAACA 192

DB 43 IleThrCysArgalaSerGlnGlyIleSerArgLeuLeuAlaTrpTrpGlnGlnIlePro 62  
 QY 193 GGTAAGACCTTAAGCTCCGATCTATGTCAGATCCAGTTTGCAAGAGTGCCCACTCA 252  
 DB 63 GlyValaIleProIleLeuLeuIleTrpValaIleSerSerLeuGlnSerGlyValProSer 82  
 QY 253 AGTTTCAGCCGAGATGATCTGGACAGATTTTCACTTCACCATCAGACCTGACAGCCT 312  
 DB 83 ArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 102  
 QY 313 GAAGATTTTGCACTTCTATTTGTCACAGGCTAAATAGTTTCCCGTACATTTTGGTCAG 372  
 DB 103 GlnAspPheAlaThrTrpTrpCysGlnGlnAlaAsnSerPheProTrpTrpPheGlyGln 122  
 QY 373 GGAACCAAGCTGAGATCAACAGAACTGTCGTCACCATCTGCTTC 420  
 DB 123 GlyThrIleValGlnIleIleValArgThrValaIleAlaProSerValaIle 138

RESULT 2

ID AAB82912 standard; Protein; 241 AA.

AC AAB82912;

DT 26-NOV-2001 (first entry)

DE Human immune response protein HIRP1.

XX  
 XX Immune response protein; HIRP1; human; immunological disease;  
 KW cell proliferation; cancer; anti-HIV; antiallergic;  
 KW antianemic; antidiabetic; antiarteriosclerotic; antipneumatic;  
 KW immunosuppressive; dermatological; antidiabetic; antiinflammatory;  
 KW neuroprotective; osteopathic; antineumatic; antiallergic;  
 KW antitumor; virucide; antibacterial; fungicide; protozoacide;  
 KW antihelminthic; vulnerary; hepatotropic; cytostatic; therapy;  
 KW diagnosis; vaccine; immunoglobulin.  
 XX  
 OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= Signal\_peptide  
 FT Protein 22..241  
 FT /label= Mature\_protein  
 FT Modified-site 36  
 FT /note= "O-phosphorylated"  
 FT Modified-site 44  
 FT /note= "O-phosphorylated"  
 FT Modified-site 79  
 FT /note= "O-phosphorylated"  
 FT Modified-site 80  
 FT /note= "O-phosphorylated"  
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 FT Modified-site 94  
 FT /note= "O-phosphorylated"  
 FT Modified-site 129  
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 FT Modified-site 191  
 FT /note= "O-phosphorylated"  
 FT Modified-site 209  
 FT /note= "O-phosphorylated"  
 FT Domain 38..117  
 FT /note= "immunoglobulin domain motif"  
 FT Region 98..134  
 FT /note= "T-cell glycoprotein CD8 motif"  
 FT Domain 123..240  
 FT /note= "immunoglobulin kappa complex motif"  
 FT Region 154..223  
 FT /note= "immunoglobulin domain motif"  
 FT Region 219..225  
 FT /note= "Ig MHC motif"  
 FT Region 197..240





FT Region /note="immunoglobulin and MHC protein motif"  
 FT 158..180 /note="immunoglobulin and MHC protein motif"  
 FT Region 219..236 /note="immunoglobulin and MHC protein motif"  
 FT MO200168696-A1.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 15-MAR-2001; 2001WO-US08518.  
 XX  
 PR 15-MAR-2000; 2000US-189417P.  
 XX  
 PA (INCYTE GENOMICS INC.  
 XX  
 PI Tang YT, Hillman JL, Baughn MR;  
 XX  
 DR WPI; 2001-590044/66.  
 DR N-PSDB; AAH26799.  
 XX  
 PT Novel human immune response proteins, for treating immunological  
 PT disorders and cell proliferative disorders, and for assessing the  
 PT effects of exogenous compounds on the expression of HIRP molecules  
 PS  
 PS Claim 1, Page 85; 95pp; English.  
 CC  
 CC The invention is based on the discovery of new human immune  
 CC response proteins (HIRP), the polynucleotides encoding them, and  
 CC the use of these compositions for the diagnosis, treatment or  
 CC prevention of immunological and cell proliferative disorders.  
 CC The present sequence is that of human immune response protein 1  
 CC (HIRP1, Incyte ID No. 6100311CD1), as determined from a  
 CC polynucleotide assembled e.g. from a lung adenocarcinoma cDNA  
 CC library clone. The amino acid sequence shows homology, from  
 CC residue W123 to C241, to an HIV-1 antigen binding protein, and  
 CC further homologues suggest that it may be an immunoglobulin. HIRP  
 CC polynucleotides and polypeptides are useful for the diagnosis,  
 CC treatment and prevention of cell proliferative disorders (e.g.  
 CC cancers, arteriosclerosis, actinic keratosis, burns, mixed  
 CC connective tissue disease (MCTD), myelofibrosis, psoriasis,  
 CC leukaemia, hepatitis, cirrhosis and atherosclerosis), and  
 CC immunological disorders e.g. AIDS, Addison's disease, adult  
 CC respiratory distress syndrome (ARDS), anaemia, asthma, autoimmune  
 CC diseases, contact dermatitis, diabetes mellitus, cholecystitis,  
 CC Crohn's disease, atrophic gastritis, Goodpasture's syndrome,  
 CC multiple sclerosis, irritable bowel syndrome, osteoporosis,  
 CC rheumatoid arthritis, ulcerative colitis, trauma, and viral,  
 CC bacterial, fungal, parasitic, protozoal and helminthic infections.  
 CC The polypeptides are also used to screen for agonist and  
 CC antagonist compounds of therapeutic use.  
 XX  
 SQ Sequence 241 AA;  
 Alignment Scores:  
 Pred. No.: 5,28e-58 Length: 241  
 Score: 621.50 Matches: 119  
 Percent Similarity: 92.20% Conservative: 11  
 Best Local Similarity: 84.40% Mismatches: 6  
 Query Match: 81.67% Indels: 5  
 DB: 22 Gaps: 1  
 US-08-728-463B-220 (1-420) x AAB82912 (1-241)  
 QY 13 ATGATGTCCTCCAGCTCAAGCTCTCGTCTGCTGCTGCTCCAGGTTCCAGATGC 72  
 DB 3 MetaxValaProlaInLeuEnglyLeuLeuLeuTrrPleuProGlyAlaIysCys 22  
 QY 73 GACATCCAGATGACCGAGTCTCCATCTCGTGTGATCTGTGGAGACAGATCCACC 132  
 DB 23 AspIleGlnMetThrInserProSerTrnLeuSerAlaSerValGlyAspArgValThr 42  
 QY 133 ATCACTTGTGGGCGAGTCAGATATTAGC-----AGCTGTAGACTGTG 177

DB 43 ILeThrYsaAlaSerGlnSerInSerSerSerInSerIleGlySerTrpLeuAlaTrp 62  
 QY 178 TATCAGATTAACCGAGTAAAGCAGCTTACCTCTGATCTTATGCTGATCCAGTTGCA 237  
 DB 63 TyrGlnGlnIlyProGlyIlyAlaProIlyLeuLeuIleTyrIlyAlaSerSerLeuGlu 82  
 QY 238 AGTGTGTCCTCCATCAAGTTCACGCGAAGATCTTGGGACAGATTTCACTTCACCATC 297  
 DB 83 SerGlyAlaProSerArgPheSerGlySerGlySerGlyThrGlnPheTrnLeuTrnIle 102  
 QY 298 AGCAGCTGCAGCCTGAGATTTTGGCACTTACTATTGTCAACAGGCTAATAGTTCCCG 357  
 DB 103 SerSerIleuGlnProAspArgPheAlaTrnTyrTyrCysGlnGlnIlyrAsnAsnTyrPro 122  
 QY 358 TACACTTTGTGTCAGGAGACCAAGCTGTGAGATTAACGAACTGTGCTGCACCATCTGTC 417  
 DB 123 TrpThrPheGlyIlyGlnIlyThrIlySerValGluIleIlyArgThrValAlaIleProSerVal 142  
 QY 418 TTC 420  
 DB 143 Phe 143  
 RESULT 3  
 AAR38162  
 ID AAR38162 standard; Protein; 234 AA.  
 XX  
 AC AAR38162;  
 XX  
 DT 01-OCT-1993 (first entry)  
 XX  
 DE Sequence of the kappa light chain variable region (VK) of human  
 DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line  
 XX 88Bv59, ATCC CRL 10624.  
 XX  
 KW B-cell; immunoglobulin g; cancer; tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..214  
 FT /tag= a  
 FT /label= 1st AA denoted AA#1  
 FT 24..49  
 FT /tag= b  
 FT /label= CDR 1  
 FT 50..88  
 FT /tag= c  
 FT /label= CDR 2  
 FT 89..108  
 FT /tag= d  
 FT /label= CDR 3  
 FT 109..214  
 FT /tag= e  
 FT /label= CON  
 XX  
 XX EP546634-A.  
 XX  
 XX 16-JUN-1993.  
 XX  
 XX 09-DEC-1992; 92EP-0203827.  
 XX  
 XX 13-DEC-1991; 91US-0807300.  
 XX  
 XX (ALKO) AKZO NV.  
 XX  
 XX Crichton VZ, Haspel MV, Kobrin BJ;  
 DR WPI; 1993-190019/24.  
 DR N-PSDB; AA043773.  
 XX  
 PT Transformed human B-cell line for monoclonal antibody prodn. for  
 PT cancer diagnosis - prepd from peripheral blood B-cells of cancer

```

Db      83  ArgPheSerGIySerGIySerGIyThraSPheThrLeuThrIleSerSerLeuGlnPro 102
Qy      313 GAAGATTTTGCACTTACTATTGTCAACAGAGCTATATGTTTC--CCGTACACTTTTGGT 369
Db      103 GlnaSPheIaThrIyTyTyTyGlnGlnSerIySerIyThrProProlIeThrPheGly 122
Qy      370 CAGGGAACCAAGCTGAGATCAACGAACTGTGGCTGCACCATCTGCTTC 420
Db      123 GlnGIyThraArgLeuGlnIleIyArgThraValaIaIaIaProSerValPhe 139

RESULT 5
AAy96289
ID      AAY96289 standard; protein; 237 AA.
XX
AC      AAY96289;
XX
DT      16-AUG-2000 (first entry)
XX
DE      Human IGFAM-1 immunoglobulin.
XX
KM      Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;
XX      infection; inflammation; haematopoiesis; AIDS; allergy.
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Peptide    1..22
FT      Protein    /label= signal_peptide
FT      Protein    23..237
FT      Protein    /label= IGFAM-1
FT      Domain     38..112
FT      Domain     /label= Ig_domain
FT      Domain     150..219
FT      Domain     /label= Ig_domain
FT      Region     154..176
FT      Region     /label= Ig_signature
FT      Domain     193..236
FT      Domain     /label= Ig_domain
FT      Region     215..232
FT      Region     /label= Ig_signature

XX      WO200029583-A2.
XX      25-MAY-2000.
XX
PF      19-NOV-1999; 99MO-US27566.
XX
PR      19-NOV-1998; 99US-0113635.
PR      22-DEC-1998; 98US-0113635.
PR      07-APR-1999; 99US-0128194.
XX
PA      (INCY-) INCYTE PHARM INC.
XX
PI      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI      Lu DM, Lal P, Hillman JL, Yang J;
XX
XX      WPI: 2000-387796/33.
XX      N-PSDB; AAA27381.
XX
DR      N-PSDB; AAA27381.
XX
XX      Claim 1; Page 77-78; 105pp; English.
XX
XX      The present sequence is the human immunoglobulin superfamily protein
XX      IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane
XX      tissue. It is expressed in reproductive, gastrointestinal and
XX      cardiovascular tissue, where cancer and inflammation are common. The
XX      gene, protein, its antibodies, agonists and antagonists are suitable for
XX      diagnosing and treating many diseases, including cancer, immune system

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CC      disorders (such as inflammation, AIDS, allergies, anaemia,
CC      atherosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC      systemic lupus erythematosus and ulcerative colitis), complications of
CC      cancer, haemodialysis and extracorporeal circulation, trauma and
CC      haematopoietic cancer (such as leukaemia) and infections caused by
CC      bacteria, viruses, fungi or parasites.
XX
SQ      Sequence 237 AA:
XX
XX      Alignment Scores:
XX      Pred. No.: 2,13e-56 Length: 237
XX      Score: 606.50 Matches: 121
XX      Percent Similarity: 91.97% Conservative: 5
XX      Best Local Similarity: 88.32% Mismatches: 10
XX      Query Match: 79.70% Indels: 1
XX      DB: 21 Gaps: 1

US-08-728-463b-220 (1-420) x AAY96289 (1-237)

Qy      13  ATGATGTCCTCCAGCTCAGCTCCCTCGGTCCTCGTCTGTTCCAGGTTCCAGATGC 72
Db      3  MetArgValProIaGlnLeuLeuGlyLeuLeuLeuThrPheuArgIyAlaArgCys 22
Qy      73  GACATCCAGATGACCCAGTCTCCATCTCCGTCGTGCATCTGTAGAGACAGAGTCACC 132
Db      23  AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 42
Qy      133  ATCACTTTGGGGCGAGCTACGATATTAGACGCTGGTTAGCCTGTTACGATTAACCA 192
Db      43  IleThrCysArgIaGlnIleSerIleSerSerTyLeuAsnThrTyGlnGlnIlyPro 62
Qy      193  GGTAAAGACCTAAGCTCCGATCTATCTATGTCATCTGATGGAAGTGGTGTCACATCA 252
Db      63  GlyValaIaProIySneueuIleTyAlaAlaSerSerLeuGlnSerGlyValProSer 82
Qy      253  AGGTTACGCGAAGTGAATCTGGAGACGATTTCACTTCAACATCAGACCTGCAGCCT 312
Db      83  ArgPheSerGIySerGIySerGIyThraSPheThrLeuThrIleSerSerLeuGlnPro 102
Qy      313 GAAGATTTTGCACTTACTATTGTCAACAGAGCTATATGTTTC--CCGTACACTTTTGGT 369
Db      103 GlnaSPheIaThrIyTyTyTyGlnGlnSerIySerIyThrProProlIeThrPheGly 122
Qy      370 CAGGGAACCAAGCTGAGATCAACGAACTGTGGCTGCACCATCTGCTTC 420
Db      123 GlnGIyThraArgLeuGlnIleIyArgThraValaIaIaIaProSerValPhe 139

RESULT 6
AAy96301
ID      AAY96301 standard; protein; 237 AA.
XX
AC      AAY96301;
XX
DT      16-AUG-2000 (first entry)
XX
DE      Human IGFAM-13 immunoglobulin.
XX
KM      Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
XX      infection; inflammation; haematopoiesis; AIDS; allergy.
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      Peptide    1..22
FT      Protein    /label= signal_peptide
FT      Protein    23..237
FT      Protein    /label= IGFAM-13
FT      Domain     38..112
FT      Domain     /label= Ig_domain
FT      Domain     150..219
FT      Domain     /label= Ig_domain

```

FT	Domain	193..236
FT	/Label= Ig_domain	
XX		
PN	WO200029583-A2.	
PD	25-MAY-2000.	
PF	19-NOV-1999;	99MO-US27566.
PR	19-NOV-1998;	99US-0113635.
PR	22-DEC-1998;	98US-0113635.
PR	07-APR-1999;	99US-0128194.
XX	(INCY-) INCYTE PHARM INC.	
PA		
PI	Yue H, Tang YT, Corley NC, Guesler KI, Gorgone GA, Baughn MR,	
PI	Lu DM, Lai P, Hillman JL, Yang J;	
DR	WPI; 2000-387796/33.	
DR	N-PSTDB; AAA27393.	
PT	Immunoglobulin superfamily proteins, the agonist and antagonist of the	
PT	protein is useful for preventing and treating disorders associated with	
PT	altered levels of the protein such as cancer, immune system disorders	
PT	-	
XX		
PS	Claim 1; Page 87-88; 105pp; English.	
CC	The present sequence is the human immunoglobulin superfamily protein	
CC	IGFAM-13. Its gene was isolated from a cDNA library of lung tumour	
CC	tissue. It is expressed in reproductive, gastrointestinal and	
CC	cardiovascular tissue, where cancer and inflammation are common. The	
CC	gene, protein, its antibodies, agonists and antagonists are suitable for	
CC	diagnosing and treating many diseases, including cancer, immune system	
CC	disorders (such as inflammation, AIDS, allergies, anaemia,	
CC	arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's	
CC	disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,	
CC	multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,	
CC	systemic lupus erythematosus and ulcerative colitis), complications of	
CC	cancer, hemodialysis and extracorporeal circulation, trauma and	
CC	haematopoietic cancer (such as leukaemia) and infections caused by	
CC	bacteria, viruses, fungi or parasites.	
SQ	Sequence 237 AA;	
<hr/>		
Alignment Scores:		
Pred. No.:	2,13e-56	Length: 237
Score:	606.50	Matches: 119
Percent Similarity:	93.43%	Conservative: 9
Best Local Similarity:	86.86%	Mismatches: 8
Query Match:	79.70%	Indels: 1
DB:	21	Gaps: 1
<hr/>		
US-08-728-463B-220 (1-420) x AAY96301 (1-237)		
QY	13 ATGATGTCTCCAGTCAAGTCCTCGGTCTGGTTCCAGATTCCAGATGC	72
Dd	3 MetatrgalprolaaglnleuleuglyneuleuleutripLeuarglYAlarGys	22
QY	73 GACATCCAGATGAACCAAGTCTCATCTTCGTTGTCATCTGTAGAGAGAAGATCAC	132
Dd	23 AsplleglnmetrhnglnserProserSerleuSerAlaserValGlYAspargValthr	42
QY	133 ATCACCCTGTGGGGCGAGTCAAGATATTATACACTGGTTAAGCTGGTATCAGATPAA	195
Dd	43 MetrhCyarYgalAaserGlnserIlleSerThrTYrLeuAasrrTPYrGlInglYalPro	62
QY	193 GTTAAAGACACTTAAGCTCTGTATCTATAGCTGCATCAAGTTTGCAAAGGAGTCCATCA	255
Dd	63 GlyLylalAProlysleuLeuIleTYrAlaAlaserSerleuGlnserGlyValProser	82
QY	253 AGGTTCAGGGGAAGTGATCTGGACAGATTTCATCTTCACCATCAGACGCTTGACCTT	312

Db	83	ArgpheeerclgyserrclgyserrclgylthAspPheThrLeuThrIleSerSerLeuGlnPro	102
Qy	313	GAGATTTCGCACTTACTTACTTTCGACAGAGCT---ATAAGTTTCCCGTACACTTTTGGT	369
Db	103	GluAspPheAlaThrTrpCysGlnGlnSerPheAsnThrHISmetCylrthPheGly	1222
Qy	370	CAGGAACACAGAGCGAGATCAACAGACCTGTGGCTGCACACTGTCTTC	420
Db	123	GlnCylrthArgLeuGlnuMetCylsArgTrhValAlaAlaProSerValPhe	139
RESULT 7			
ABP43157			
ID	ABP43157	standard; Protein; 139 AA.	
XX	AC	ABP43157;	
XX	DT	22-AUG-2002 (first entry)	
XX	DE	Human ovarian antigen HVC150, SEQ ID NO:4289.	
XX	KM	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;	
KM	KM	ovarian cancer; breast cancer; tumour; reproductive system disorder;	
KM	KM	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;	
KM	KM	PCOS; ovarian cysts; dysmenorrhoea; endocrine disorder; infection;	
KM	KM	inflammatory condition; immune disorder; blood disorder;	
KM	KM	cardiovascular disorder; respiratory disorder; neurological disorder;	
KM	KM	gastrointestinal disorder; urinary system disorder; drug screening;	
KM	KM	gene therapy; chromosome mapping; forensic analysis;	
KM	KM	antibody preparation; cytostatic; immunomodulatory; neuroprotective;	
KM	KM	antiinflammatory; gynaecological; reproductive.	
XX	OS	Homo sapiens.	
XX	PN	WO200200677-A1.	
XX	PD	03-JUN-2002.	
XX	PF	07-JUN-2001; 2001WO-US18569.	
XX	PR	07-JUN-2000; 2000US-209467P.	
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PI	Birce CE, Rosen CA;	
XX	DR	WPI; 2002-147878/19.	
XX	DR	N-PSDB; AB056234.	
PT	PT	Isolated nucleic acid molecules encoding novel ovarian polypeptides,	
PT	PT	useful in the prevention, treatment and diagnosis of cancer (e.g.	
PT	PT	ovarian cancer), immune disorders, cardiovascular disorders and	
PT	PT	neurological diseases -	
XX	XX	Claim 11; SEQ ID No 4289; 2922pp; English.	
XX	XX		
CC	CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-	
CC	CC	ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
CC	CC	encompasses polypeptides 90% identical and polynucleotides 95% identical	
CC	CC	to the sequences of the invention. The invention additionally relates to	
CC	CC	recombinant vectors and host cells comprising human ovarian antigen	
CC	CC	polynucleotides, antibodies against human ovarian antigens, and the use	
CC	CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,	
CC	CC	treating, prognosing or preventing various ovary and/or breast-related	
CC	CC	disorders. Such conditions include ovarian cancer and breast cancer, and	
CC	CC	metastatic tumours of ovarian or breast origin, reproductive system	
CC	CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,	
CC	CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	
CC	CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	
CC	CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	
CC	CC	vaginitis), immune disorders (e.g., congenital and acquired	
CC	CC	immunodeficiencies, autoimmune oophoritis), systemic lupus erythematosus),	
CC	CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,	
CC	CC	respiratory disorders, neurological disorders, gastrointestinal disorders	

CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 CC  
 XX

SO Sequence 139 AA;  
 Alignment Scores:  
 Pred. No.: 5.6e-56 Length: 139  
 Score: 602.00 Matches: 113  
 Percent Similarity: 90.98% Conservative: 8  
 Best Local Similarity: 84.96% Mismatches: 11  
 Query Match: 79.11% Indels: 1  
 DB: 23 Gaps: 0

US-08-728-463b-220 (1-420) x ABP43157 (1-139)

QY 19 GTCCAGCTCAGCTCTCTGCTCTCTGCTCTGCTCCAGGTTCCAGATGCGATC 78  
 |||||  
 DB 2 ValProAla\*\*\*LeuLeuGlyLeuLeuLeu\*\*\*LeuProGlyAlaIysCysAspIle 21  
 |||||  
 QY 79 GAGATACCCAGTCTCCATCTTCGCTGCTGATCTGTAGAGACAGAGTCCACCATC 138  
 |||||  
 DB 22 GlnMetThrGln\*\*ProSerThrLeuSerAlaSerValGlyAspArgValThrIleThr 41  
 |||||  
 QY 139 TGTGGGCGAGTATAGAGATTTAGAGCTGTTAGCTGATACAGATTAACAGATAA 198  
 |||||  
 DB 42 CysArgAla\*\*GlnSerIleSerSerTrp\*\*AlaThrPyrGlnGlnIlyProGlyLys 61  
 |||||  
 QY 199 GCACTTAAGTCTGATCTATATGCTGCATCCAGTTTGAAGTGCTGCCATCAAGTTC 258  
 |||||  
 DB 62 AlaProIyLeuLeuIleIytr\*\*\*AlaSerSerLeuGlnSerGlyValProSerArgPhe 81  
 |||||  
 QY 259 AGGGAAGTGGATCTGGAGACATTTGATCTCCATCCAGCCTCGACCTGGAAGAT 318  
 |||||  
 DB 82 SerGlySerIlySerGlyThrGlnPheThrLeuThrIleSerSerLeuGlnProAspAsp 101  
 |||||  
 QY 319 TTGCAACTTACTATTTGTCAACAGAGGTAATAGTTTCCCGACACTTTGGTCAGGAGAC 378  
 |||||  
 DB 102 PheAlaThrIyTrIyCysGlnHisIyTrAsnSerIyTrProIyThrPheGlyGlnGly-Pr 121  
 |||||  
 QY 379 AAGCTGGAGATCAAAAGCAACTGTGGCTGCACCATCTG 415  
 |||||  
 DB 121 oSerTrpArgSerAsnGlnIleuTrpLeuHisHisIleu 133  
 |||||

RESULT 8  
 ABP41164  
 ID ABP41164 standard; Protein; 260 AA.  
 XX  
 AC ABP41164;  
 XX

DT 23- AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HRACM30, SEQ ID NO:2296.  
 XX  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KM ovarian cancer; breast cancer; reproductive system disorder;  
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KM inflammatory condition; immune disorder; blood disorder;  
 KM cardiovascular disorder; respiratory disorder; neurological disorder;  
 KM gastrointestinal disorder; urinary system disorder; drug screening;  
 KM gene therapy; chromosome mapping; forensic analysis;  
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KM antiinflammatory; gynaecological; reproductive; chromosome 2p12.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WPI; 2002-147878/19.  
 XX  
 DR N-PsDB; AB054241.  
 XX

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
 PT ovarian cancer), immune disorders, cardiovascular disorders and  
 PT neurological diseases -  
 XX

PS Claim 11, SEQ ID No 2296; 29222P; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 XX

SO Sequence 260 AA;

Alignment Scores:  
 Pred. No.: 8.47e-56 Length: 260  
 Score: 601.00 Matches: 117  
 Percent Similarity: 91.18% Conservative: 7  
 Best Local Similarity: 86.03% Mismatches: 12  
 Query Match: 78.98% Indels: 0  
 DB: 23 Gaps: 0

US-08-728-463b-220 (1-420) x ABP41164 (1-260)

QY 13 ATGATGATCCAGCTCAGCTCTCTGCTCTCTGCTGTTCCAGGTTCCAGATGC 72  
 |||||  
 DB 27 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuArgGlyAlaArgCys 46  
 |||||  
 QY 73 GACATCCAGATGACCCAGTCTCATCTTCGCTGCTGATCTGTAGAGACAGAGTCCAC 132  
 |||||  
 DB 47 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 66  
 |||||

QY 133 ATCACTGTGGGCGAGTCAAGATATTAGCAGCTGCTTACCTGCTATCCATTAACCA 192  
 DB 67 IlerhrysaRgaIaSerGlnSerIleSerAsnIleuSerantiPyrGlnGlnPro 86  
 QY 193 GGTAAACCACTTAAGCTCTGCTATGCTGATCCAGTTTGCAAGTGGTGCATCA 252  
 DB 87 GlyValaProIyaleuIleTyAlaIaSer\*\*LeuGlnSerGlyAlaProSer 106  
 QY 253 AGGTTTCAAGAGTGAATCTGGAGAGATTTTACCTCTCAAGCTGACGCT 312  
 DB 107 ArgPheSerGlySerGlyThrAspPheThr\*\*ThrIleSerSerLeuGlnPro 126  
 QY 313 GAAGATTTTCAACTTACTATTGCTCAACAGGCTATAGTTCCGACACTTTGGTGC 372  
 DB 127 GluAspPheAlaThrTyTrpGlnGlnIlyAspAsn\*\*ProLeuThrPheGly\*\*\* 146  
 QY 373 GGAACCAAGCTGAGATCAACAGAACTGTGGCTGCACCATCTGTCTTC 420  
 DB 147 GlyThrIyValGlnIleIySaRgThrValAlaIaIaProSerValPhe 162

RESULT 9  
 AAR20058  
 ID AAR20058 standard; Protein; 234 AA.

XX AC AAR20058;  
 XX 25-MAR-1992 (first entry)  
 DE Light chain of 3D6 anti-HIV antibody.  
 XX Plasmid pUC3D6LC; human immunodeficiency virus; AIDS;  
 KM complementarity determining region.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= signal  
 FT Protein 23..234  
 FT Region 23..45  
 FT /label= Framework\_1  
 FT 46..56  
 FT /label= CDR\_1  
 FT 57..71  
 FT /label= Framework\_2  
 FT 72..78  
 FT /label= CDR\_2  
 FT 79..110  
 FT /label= Framework\_3  
 FT 111..117  
 FT /label= CDR\_3  
 FT 118..127  
 FT /label= Framework\_4  
 FT 128..234  
 FT /label= Constant\_region

XX WO9118983-A.  
 XX 12-DEC-1991.  
 PD 28-MAY-1991; 91WO-1000067.  
 XX 29-MAY-1990; 90AT-0001178.  
 XX (JUNG/) JUNGSAUER A.  
 XX Feigenhauer M, Himmeler G, Kohl J, Steindl F;  
 XX WPI; 1992-007468/01.  
 DR N-PSDB; AAQ20067.  
 XX  
 PT Recombinant protein which binds to complex viral antigen and

PT HIV-1 - contains variable region of antibody derived from 3D6  
 PT cell line, used for detecting HIV-1 antigen  
 XX  
 PS Claim 3; Page 28; 52pp; German.  
 XX  
 CC The variable region of the light chain is used in a recombinant  
 CC protein with the variable region from the heavy chain of 3D6,  
 CC the two V regions being joined by a linker. The recombinant  
 CC protein binds to HIV gp160.  
 CC See also AAQ20066 and AAQ20068.  
 XX  
 SQ Sequence 234 AA;

Alignment Scores:  
 Pred. No.: 1,35e-55 Length: 234  
 Score: 599.00 Matches: 115  
 Percent Similarity: 91.91% Conservative: 10  
 Best Local Similarity: 84.56% Mismatches: 9  
 Query Match: 78.71% Indels: 2  
 DB: Gaps: 13

US-08-728-463B-220 (1-420) x AAR20058 (1-234)

QY 13 ATGATGTCCTCCAGCTCAGCTCCGCTGCTCTGCTGTTCCAGCTTCCAGATCC 72  
 DB 3 MetArgValProAlaGlnLeuGlyLeuLeuLeuLeuProGlyAlaIyScys 22  
 QY 73 GACATCCAGATGACCCAGTCTCCATCTCCGTCGTCGATCGTAGAGACAGATCACC 132  
 DB 23 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr 42  
 QY 133 ATCACTGTGGGCGAGTCAAGATATTAGCAGCTGTTAGCTGGTATCAGATTAACCA 192  
 DB 43 IlerhrysaRgaIaSerGlnSerIleSerArgIleuIleAlaIyPyrGlnGlnPro 62  
 QY 193 GGTAAACCACTTAAGCTCTGATCTATGCTGTCGATCCAGTTTGCAAGTGGTGCATCA 252  
 DB 63 GlyIyValProIyaleuIleTyRlySaIaSerSerLeuGlnIyAlaProSer 82  
 QY 253 AGGTTTCAAGAGTGAATCTGGAGAGATTTTACCTTCAACATGAGCCTGACGCT 312  
 DB 83 ArgPheSerGlySerGlySerGlyThrGlnPheThrIleSerSerLeuGlnPro 102  
 QY 313 GAAGATTTTCAACTTACTATTGCTCAACAGGCTATAGTTTCCGATCTTTGGTGCAG 372  
 DB 103 AspAspPheAlaThrTyTrpGlnGlnIlyAsnSer-----TyrSerPheGlyPro 120  
 QY 373 GGAACCAAGCTGAGATCAACAGAACTGTGGCTGCACCATCTGTCTTC 420  
 DB 121 GlyThrIyValaIleIySaRgThrValAlaIaIaProSerValPhe 136

RESULT 10

AAB99115  
 ID AAB99115 standard; Protein; 146 AA.

XX AAB99115;

XX 22-AUG-2001 (first entry)

XX Human protein SEQ ID 12.

XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;  
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;  
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis.  
 XX  
 OS Homo sapiens.

XX WO200136642-A1.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-JP08129.









XX AAB15546;  
 XX  
 DT 28-FEB-2001 (first entry)  
 DE Human immune system molecule from Incyte clone 1666486.  
 KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic;  
 KW antiarteriosclerotic; antistatic; antidiabetic; nephrotoxic; cancer  
 KW antipain; dermatological; antihypertoid; vitaminic; hepatotropic; antibody  
 KW immunosuppressive; cyostatic; fungicide; protozoicide; antibacterial;  
 KW gene therapy; diagnostic; immunological disorder; viral infection;  
 KW bacterial infection; fungal infection; parasitic infection; immunogen.  
 XX  
 OS Homo sapiens.  
 PN MO200060080-A2.  
 XX  
 PD 12-OCT-2000.  
 XX  
 PF 04-APR-2000; 2000WO-US09072.  
 XX  
 PR 05-APR-1999; 99US-0127852.  
 PR 05-MAY-1999; 99US-0132647.  
 PA (INCY-) INCYTE PHARM INC.  
 PI Yue H, Lai P, Tang YT, Baughn MR, Azimzai Y, Lu DM;  
 DR MPI: 2000-665005/64.  
 DR N-PSDB; AAB95785.  
 XX  
 PT New human immune system molecules 1-15 and polynucleotides encoding  
 PT them useful for diagnosing, treating or preventing e.g. immunological  
 PT disorders, infections, cell proliferative disorders, microbial  
 PT infections -  
 PS  
 PS Claim 1; Page 83-84; 95pp; English.  
 XX  
 XX This sequence represents a human immune system molecule (IMOL) encoded  
 CC by the cDNA isolated as clone 1666486 from the Incyte BMAR0703 library.  
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
 CC (AAB95775-A95789), and compositions comprising them are useful for the  
 CC diagnosis, treatment or prevention of immunological disorders,  
 CC infections and cell proliferative disorders, including cancer. The IMOL  
 CC may be used to treat or prevent disorders associated with decreased  
 CC expression or activity of IMOL, such as immunological disorders  
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,  
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,  
 CC Shigella), fungi (e.g. Aspergillus, Blastomycetes), parasites (e.g.  
 CC plasmidium, trypanosoma, intestinal protozoal), cell proliferative  
 CC disorders (e.g. actinic keratosis, arteriosclerosis, psoriasis), and  
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also  
 CC useful as immunogens for the development of antibodies that  
 CC specifically recognize these peptides. The polynucleotides may be used  
 CC to detect and quantify gene expression in biopsied tissues in which  
 CC expression of IMOL may be correlated with the disease, as targets in a  
 CC microarray, to detect differences in gene sequences among normal,  
 CC carrier and affected individuals, and for screening libraries of  
 CC compounds in drug screening techniques. Antibodies which specifically  
 CC bind to IMOL may be used for the diagnosis of disorders characterized  
 CC by expression of IMOL, or in assays to monitor patients being treated  
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.  
 XX  
 XX Sequence 237 AA;  
 XX

Alignment Scores:	
Pred. No.:	3,78e-54
Score:	585.50
Percent Similarity:	93.43%
Best local Similarity:	80.29%
Query Match:	76.94%
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Matches:	110
Conservative:	18
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US-08-728-463B-220 (1-420) x AAB15546 (1-237)

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QY      133     ATCATTTGTGGGCGAGTCAGATATTATAGACCTGGTATCGCTGGATTCAGAGTAAACA      197
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Db      103     AspAspPheMetAlaThrTyrPheCysGlnGlnTyrAspTrnTyrProTrnTrpSerPheGly      122
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DT	29-APR-1994 (first entry)
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DE	Human anti-HBs light chain.
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KW	Antibody; Ab; light; heavy; chain; hepatitis B;
XX	HB; surface antigen.
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FH	Key
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FT	1..22
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PN	W09320205-A.
PD	14-OCT-1993.
XX	
PF	30-MAR-1993; 93WO-JP00396.
XX	
PR	30-MAR-1992; 92JP-0074678.
XX	
PA	(SUNR ) SUNTORY LTD.
XX	
PI	Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
XX	
DR	WPI; 1993-336913/42.
DR	N-PSDB; AA049943.
XX	
FT	Human anti-hepatitis B surface antigen antibody gene - can be
XX	used to produce L and H chains of the antibody in large quantity
XX	Disclosure; Fig 4-5; 46pp; Japanese.

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Tue Jun 3 09:41:15 2003

us-08-728-463b-220.rag

Page 13

Db :123 GlyThrIysValGluHisLysArg 130

Search completed: June 3, 2003, 09:02:30  
Job time : 29.3328 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:04:15 ; Search time 17.8452 Seconds  
(without alignments)  
4764.744 Million cell updates/sec

Title: US-08-728-463b-220

Perfect score: 761

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 383519 segs, 101223694 residues

Total number of hits satisfying chosen parameters: 767038

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database: Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	656	86.2	236	10	US-09-859-053-30 Sequence 30, Appl
2	591	77.7	234	10	US-09-740-002-24 Sequence 24, Appl
3	567	74.5	236	9	US-10-006-593-69 Sequence 69, Appl
4	558.5	73.4	234	10	US-09-740-002-26 Sequence 26, Appl

5	548	72.0	128	10	US-09-855-271-26 Sequence 26, Appl
6	534	70.2	234	10	US-09-800-729-150 Sequence 150, App
7	529	69.5	214	9	US-10-153-382-19 Sequence 19, Appl
8	526.5	69.2	109	10	US-09-798-058-47 Sequence 4, Appl
9	524	68.9	127	9	US-10-283-349-71 Sequence 71, Appl
10	522.5	68.7	235	10	US-09-800-729-152 Sequence 152, App
11	520	68.3	214	10	US-09-940-166A-2 Sequence 2, Appl
12	520	68.3	214	10	US-09-811-384-11 Sequence 11, Appl
13	520	68.3	237	9	US-10-227-694-1 Sequence 1, Appl
14	520	68.3	237	10	US-09-940-166A-6 Sequence 6, Appl
15	518	68.1	244	9	US-09-880-748-1881 Sequence 1881, Ap
16	514	67.5	109	10	US-09-811-123-6 Sequence 6, Appl
17	514	67.5	218	10	US-09-917-410-2 Sequence 2, Appl
18	514	67.5	237	9	US-10-020-786-10 Sequence 10, Appl
19	514	67.5	237	10	US-09-056-160B-100 Sequence 100, App
20	514	67.5	491	12	US-10-011-125-2 Sequence 2, Appl
21	512	67.3	218	9	US-09-925-179-9 Sequence 9, Appl
22	512	67.3	218	10	US-09-802-077-9 Sequence 9, Appl
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26	509	66.9	127	9	US-10-283-349-88 Sequence 88, Appl
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28	509	66.9	218	10	US-09-920-171-17 Sequence 17, Appl
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34	503	66.1	218	9	US-09-925-179-67 Sequence 67, Appl
35	502	66.0	214	9	US-09-875-221A-128 Sequence 128, App
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40	501	65.8	237	9	US-10-227-694-4 Sequence 4, Appl
41	499	65.6	106	9	US-10-027-725A-12 Sequence 12, Appl
42	498	65.4	127	9	US-10-283-349-92 Sequence 92, Appl
43	498	65.4	128	10	US-09-992-524-6 Sequence 6, Appl
44	498	65.4	245	9	US-09-797-941A-6 Sequence 6, Appl
45	497	65.3	107	9	US-09-848-798-40 Sequence 40, Appl

#### ALIGNMENTS

RESULT 1  
US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. US20020102658A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Takashi  
; APPLICANT: Tezuka, Katsunari  
; APPLICANT: Hori, No. US20020102658A1uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND  
; FILE REFERENCE: PHARMACEUTICAL USE THEREOF  
; CURRENT APPLICATION NUMBER: 06501-079001  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30  
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Pred. No.:



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US-09-740-002-26			
Sequence 26, Application US/09740002			
Patent No. US20020001798A1			
GENERAL INFORMATION:			
APPLICANT: BRAMS, PETER			
APPLICANT: MORROW, PHILLIP			
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES			
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR			
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF			
FILE REFERENCE: 037003-0275759			
CURRENT APPLICATION NUMBER: US/09/740,002			
CURRENT FILING DATE: 2000-12-20			
PRIOR APPLICATION NUMBER: 09/335,697			
PRIOR FILING DATE: 1999-06-18			
PRIOR APPLICATION NUMBER: 08/488,376			
PRIOR FILING DATE: 1995-06-07			
NUMBER OF SEQ ID NOS: 27			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 26			
LENGTH: 234			
TYPE: PR			
ORGANISM: Homo sapiens			
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QY	133	ATCACTTGTGGGCGAGTCAGATATTATTCACAGCTGGTAGCTGGTATTCACATPAAACA	193
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RESULT 5			
US-09-855-271-26			
Sequence 26, Application US/09855271			
Patent No. US20020042089A1			
GENERAL INFORMATION:			
APPLICANT: Bodmer, Mark W			
APPLICANT: Athwal, Diljeet Singh			
APPLICANT: Emtage, John Spencer			
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies			
FILE REFERENCE: CARP-0088			
CURRENT APPLICATION NUMBER: US/09/855,271			
PRIOR FILING DATE: 2001-05-15			
PRIOR APPLICATION NUMBER: 09/347,061			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 26			
LENGTH: 128			
TYPE: PRT			
ORGANISM: Artificial Sequence			
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Qy	133	ATACATCTTCGGCGGCGAGTACAGATATTTAGACAGCTGGTATGCGCTGTATCAGATAAACA	1922
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QY 253 AGGTTCAGCGAAGTGGATCTGGACAGATTTCACCTCCACATCAACACACCGTCGAGCCT 312  
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QY 313 GAAGATTTTGGCACTTACTATTTGTGCACAGGCTAATAGTTTCCGTACACTTTGGTCAG 372  
Db 101 AspAspValAlaThrTyrSerCysGlnGlnIlyrAsnThrPheProLeuThrPheGly\*\*\* 120

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RESULT 7  
US-10-153-382-19 / Sequence 19, Application US/10153382  
Publication No. US20030086930A1  
GENERAL INFORMATION:  
APPLICANT: PRIZER PRODUCTS INC.  
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
FILE REFERENCE: PC23019A  
CURRENT APPLICATION NUMBER: US/10/153,382  
CURRENT FILING DATE: 2002-05-22  
PRIOR FILING NUMBER: 60/293042

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Query Match:	69.51%
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Matches:	19
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QY	133	ATCACCTTGTGGGCGCAGTCAGAGATTTAGCAGCTGGTTAGCTGTATCAGATAAACCA	192
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QY	193	GGTAAAGACACCTAAGCTCTGATCTAAGCTGATCCAGTTTGGAAAGTGGTGCCATCA	252
Db	41	GlyIlyAlaProIlyLeuLeuIleIleThrAlaIaSerSerLeuInsIleGlyAlaProSer	60
QY	253	AGCTTCAGGGGAAGTGGATCTGGGACAGATTTCACTCTCAACATCAGACGCTGCAGCT	312
Db	61	ArgPheSerGlySerGlySerGlyIleThaAspPheThrIleuThrIleSerSerLeuGlnPro	80
QY	313	GAGATTTTGGCAACTACTATATTGTCACACAGGCTAATAGTTTCCCGACATTTTGGTCAG	372
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RESULT 8  
US-09-79

; Sequence 4, Application US/09798058  
; Patent No. US20020098523A1  
; GENERAL INFORMATION

; APPLICANT: Vaughan, Tristan John  
 ; APPLICANT: Wilton, Alison Jane  
 ; APPLICANT: Smith, Stephen  
 ; APPLICANT: Main, Sarah Helen  
 ; TITLE OF INVENTION: Human antibodies against ectoxin and their use  
 ; PRIORITY REFERENCE: A4632.000100

PRIOR APPLICATION NUMBER: US 60/187,246

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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ORGANISM: Homo sapiens  
US-09-798-058-4

Alignment Scores:	
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Percent Similarity:	97.2%
Best Local Similarity:	95.4%
Query Match:	69.1%
gaps:	10
Gaps:	1
length:	109
Matches:	104
Conservative:	2
Mismatches:	2
Indels:	1
Gaps:	1



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US-08-728-463B-220 (1-420) x US-09-798-058-4 (1-109)

OY 73 GACATCCAGATATACCCAGCTCCATCTTCGCGTCTGCATCTGTAGAGACAGAGTCACC 132
Db 1 AApIleGIeImeTtHrCInSerProSerSerValSerAlaSerIeugInSerGlyAlaProValThr 20
OY 133 ATCACTTGTCGGGCGAGTCAGAGATATTAGACGTGGTGAAGCCGTGATTCAGCATAAACA 192
Db 21 IletHrCySArAlaSerGlnApeIleSerSerTripleuAlaTrpPyrGlnGlnIysPro 40
OY 193 GGTAAAGACCCCTAAGCTCCTGATCTATAGCTGCATCCAGTTTGCAAGTGTGTCCTCATCA 252
Db 41 GlyValAlaProIysLeuLeuIeTyrAlaAlaSerSerIeugInSerGlyAlaProSer 60
OY 253 AGCTTCAGCGGAAGTGCATCTGGGACAGATTTTACTCTCACCATCAGACCTGCACCT 312
Db 61 ArpIleSerGlySerIylSerGlyThrArpPheThrLeuThrIleSerSerIeugInPro 80
OY 313 GAAGATTTTGCAACTTACTATTGTCAACAGCGCTAATAGTTCCCG--TACACTTTGGT 368
Db 81 GluArpPheAlaThrTyrTyrCysGlnGlnAlaSerSerPheProSerIleTrpPheGly 1000
OY 370 CAGGGAACCCAGCTGGAGATCAACGA 396
Db 101 GlnGlyThrArgLeuGlnIleIysAlaGly 109

RESULT 9
US-10-283-349-71
; Sequence 71, Application US/10283349
; Publication No. US20030096977A1
; GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiho
NAKAMURA, Kazuyaasu
IIDA, Akihito
ANAZAWA, Hideharu
HANAI, No. US20030096977A1uo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:

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REFERENCE/DOCKET NUMBER: P1729C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-811-384-11

Alignment Scores:  
Pred. No.: 2,45e-37 Length: 214  
Score: 520.00 Matches: 100  
Percent Similarity: 93.10% Conservative: 8  
Best Local Similarity: 86.21% Mismatches: 8  
Query Match: 68.33% Indels: 0  
DB: 10 Gaps: 0

US-08-728-463B-220 (1-420) x US-09-811-384-11 (1-214)

QY 73 GACATCCAGATGACCCAGTCTCCGTCGTCATCTGTAGAGAGACAGTCCACC 132  
DB 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 20  
QY 133 ATCACTTTCGGCGAGTCAAGATATTAGCAGCTGTAGCTGTATCAGCATTAACCA 192  
DB 21 IleThrCysArgAlaSerGlnAspIleAsnAsnTrpLeuAsnTrpGlnGlnPro 40  
QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCGATCCAGTTGCAAGGTGTGCCATCA 252  
DB 41 GlyValAlaProIleLeuLeuIleTrpThrSerThrLeuHisSerGlyValProSer 60  
QY 253 AGGTTCAGCGGAGTGTATTTGACACGATTTCACTCCACCATCAGACCTTGCCACT 312  
DB 61 ArgPheSerGlySerGlySerGlyThrAspTrpThrLeuThrIleSerSerLeuGlnPro 80  
QY 313 GAAGATTTCGCACTTACTATTGTCAACAGAGCTATAGTTCCCGTACCTTTGTCTGAC 372  
DB 81 GluAspPheAlaThrTrpTrpCysGlnGlnGlyAsnThrLeuProProthrpneGlyGln 100  
QY 373 GGAACCAAGCTGGAGATCAACGAAGCTGGCTGACCATCTGTCTTC 420  
DB 101 GlyThrValGluIleValArgThrValAlaAlaProSerValPhe 116

RESULT 13  
US-10-227-694-1  
Sequence 1, Application US/10227694  
Publication No. US2003007739A1  
GENERAL INFORMATION:  
APPLICANT: Simmons, Laura  
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY  
FILE REFERENCE: P1867R1  
CURRENT APPLICATION NUMBER: US/10/227,694  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: US 60/315,209  
PRIOR FILING DATE: 2001-08-27  
NUMBER OF SEQ ID NOS: 6  
SEQ ID NO 1  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-227-694-1

Alignment Scores:  
Pred. No.: 2,45e-37 Length: 237  
Score: 520.00 Matches: 100  
Percent Similarity: 93.10% Conservative: 8  
Best Local Similarity: 86.21% Mismatches: 8

Query Match: 68.33% Indels: 0  
DB: 9 Gaps: 0

US-08-728-463B-220 (1-420) x US-10-227-694-1 (1-237)

QY 73 GACATCCAGATGACCCAGTCTCCGTCGTCATCTGTAGAGAGACAGTCCACC 132  
DB 24 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 43  
QY 133 ATCACTTTCGGCGAGTCAAGATATTAGCAGCTGTAGCTGTATCAGCATTAACCA 192  
DB 44 IleThrCysArgAlaSerGlnAspIleAsnAsnTrpLeuAsnTrpGlnGlnPro 63  
QY 193 GGTAAAGCACTTAAGCTCTGATCTATGTCGATCCAGTTGCAAGGTGTGCCATCA 252  
DB 64 GlyValAlaProIleLeuLeuIleTrpThrSerThrLeuHisSerGlyValProSer 83  
QY 253 AGGTTCAGCGGAGTGTATTTGACACGATTTCACTCCACCATCAGACCTTGCCACT 312  
DB 84 ArgPheSerGlySerGlySerGlyThrAspTrpThrLeuThrIleSerSerLeuGlnPro 103  
QY 313 GAAGATTTCGCACTTACTATTGTCAACAGAGCTATAGTTCCCGTACCTTTGTCTGAC 372  
DB 104 GluAspPheAlaThrTrpTrpCysGlnGlnGlyAsnThrLeuProProthrpneGlyGln 123  
QY 373 GGAACCAAGCTGGAGATCAACGAAGCTGGCTGACCATCTGTCTTC 420  
DB 124 GlyThrValGluIleValArgThrValAlaAlaProSerValPhe 139

RESULT 14  
US-09-940-166A-6  
Sequence 6, Application US/09940166A  
Patent No. US20020058324A1  
GENERAL INFORMATION:  
APPLICANT: Blank, Gregory S.  
Narindray, Daljit S.  
Zapata, Gerardo A.  
TITLE OF INVENTION: Protein Recovery  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,166A  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/097,309  
FILING DATE: 13-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Schwartz, Timothy R.  
REGISTRATION NUMBER: 32171  
REFERENCE/DOCKET NUMBER: P1105R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-7467  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-940-166A-6



GenCore version 5.1.6  
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## OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 09:02:35 ; Search time 9.55994 Seconds  
(without alignments)  
2585.294 Million cell updates/sec

Title: US-08-728-463B-220

Perfect score: 761  
Sequence: 1 AAGCTTGCCACCATGATGCT.....TGGCTGCACCATCTGCTTC 420

Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-O=/cg2\_1/USPTO.spool/US08728463.r/unat\_03062003\_085615\_16867/app.query.fasta\_1.3690  
-DB=Issued Patents\_AA -OPMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOFC=0  
-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCLIN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US08728463 @CGN 1.1 97 @unat\_03062003\_085615\_16867 -NCPU=6 -ICPU=3  
-NO MAMP -LARGEJOB -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents\_AA.\*

- 1: /cg2\_6/ptodata/1/iaa/5A.COMB.pep.\*
- 2: /cg2\_6/ptodata/1/iaa/5B.COMB.pep.\*
- 3: /cg2\_6/ptodata/1/iaa/6A.COMB.pep.\*
- 4: /cg2\_6/ptodata/1/iaa/6B.COMB.pep.\*
- 5: /cg2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*
- 6: /cg2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585	76.9	236	1 US-08-157-101A-5	Sequence 5, Appl1
2	578	76.0	128	1 US-08-259-372A-14	Sequence 14, Appl1
3	578	76.0	128	1 US-08-468-671-14	Sequence 14, Appl1
4	562	73.9	129	1 US-08-217-918-2	Sequence 2, Appl1
5	550	72.3	233	3 US-08-812-586-45	Sequence 45, Appl1
6	548	72.0	128	2 US-08-470-139-26	Sequence 26, Appl1
7	548	72.0	128	4 US-09-347-061-26	Sequence 26, Appl1
8	541	71.1	235	3 US-08-812-586-16	Sequence 16, Appl1
9	534	70.2	128	4 US-08-569-147-80	Sequence 80, Appl1
10	528	69.4	117	4 US-09-042-353-48	Sequence 48, Appl1
11	528	69.4	117	4 US-08-758-417A-313	Sequence 313, Appl1
12	527	69.3	109	2 US-07-934-373C-3	Sequence 3, Appl1

13	527	69.3	109	3 US-08-437-642B-3	Sequence 3, Appl1
14	527	69.3	109	4 US-08-146-206C-3	Sequence 3, Appl1
15	527	69.3	109	5 PCT-US93-07833-3	Sequence 3, Appl1
16	526	69.1	127	2 US-08-621-751A-6	Sequence 6, Appl1
17	524	68.9	127	3 US-08-836-561-71	Sequence 71, Appl1
18	523	68.7	233	2 US-07-934-373C-25	Sequence 25, Appl1
19	523	68.7	233	3 US-08-437-642B-25	Sequence 25, Appl1
20	523	68.7	233	4 US-08-146-206C-25	Sequence 25, Appl1
21	523	68.7	233	5 PCT-US93-07833-25	Sequence 25, Appl1
22	522	68.6	214	2 US-07-934-373C-39	Sequence 39, Appl1
23	522	68.6	214	3 US-08-437-642B-39	Sequence 39, Appl1
24	522	68.6	214	5 PCT-US93-07833-39	Sequence 39, Appl1
25	521	68.5	116	1 US-08-053-131-185	Sequence 185, Appl1
26	521	68.5	116	2 US-08-096-762-185	Sequence 185, Appl1
27	520	68.3	214	2 US-07-934-373C-40	Sequence 40, Appl1
28	520	68.3	214	3 US-08-788-800-11	Sequence 11, Appl1
29	520	68.3	214	4 US-08-437-642B-40	Sequence 40, Appl1
30	520	68.3	214	3 US-09-097-309-2	Sequence 2, Appl1
31	520	68.3	214	4 US-09-097-171A-2	Sequence 2, Appl1
32	520	68.3	214	4 US-09-460-587-2	Sequence 2, Appl1
33	520	68.3	214	5 PCT-US93-07833-40	Sequence 40, Appl1
34	520	68.3	237	3 US-09-097-309-6	Sequence 6, Appl1
35	520	68.3	237	4 US-09-097-171A-10	Sequence 10, Appl1
36	520	68.3	237	4 US-09-422-112B-2	Sequence 2, Appl1
37	520	68.3	237	4 US-09-607-756-2	Sequence 2, Appl1
38	520	68.3	237	4 US-09-136-315-8	Sequence 8, Appl1
39	517	67.9	127	4 US-09-460-587-6	Sequence 6, Appl1
40	517	67.9	128	4 US-08-569-147-78	Sequence 78, Appl1
41	514	67.5	218	5 PCT-US96-13152-2	Sequence 2, Appl1
42	513	67.4	131	4 US-08-579-378A-18	Sequence 18, Appl1
43	513	67.4	133	1 US-08-461-284-2	Sequence 2, Appl1
44	513	67.4	133	1 US-08-462-939-2	Sequence 2, Appl1
45	513	67.4	133	1 US-08-253-877C-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-157-101A-5  
; Sequence 5, Appl1  
; Patent No. 580832  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARIANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944



OY		13	ATATGGTCCACCTAGCCTCGGATCTTCGAGCTGTGGATTCCAGATTCCAGATGC	72
Dd		3	MelArgValProIleGlnLeuGlyLeuLeuLeuLeuThrPheProGlyAlaIalysCys	22
OY		73	GACATCCAGATGAACCAGTCTCCATCTTCGATCTGCATCTGTAGAGAGACAGATCAC	132
Dd		23	AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAspArgValThr	42
OY		133	ATCACTTGTTGGGGCGAGTCAGGATATTACAGACTGGTTAGCTGGTATCCAGATTAAACA	192
Dd		43	IleThrTySarArgAlaSerGlnThrIleSerThrTrpLeuAlaTrpGlyGlnThrPro	62
OY		193	GGTAAGACCACTTAGGCTCCGTGATCTAATGCTGCATCCAGTTTGCAAGAGTGATGCCATCA	252
Dd		63	ArgIlySalAlaProLysLeuMetIleIryLySAlaSerIleLeuGlnAmGlyValProSer	82
OY		253	AGGTTCAAGCGGAAGTGGATCTGGAGACAGATTTCACCTTCACCATCAGCAGCGCTGCAGCCT	312
Dd		83	ArgPheSerGlySerGlySerGlyThrGlnPheThrLeuThrIleSerSerLeuGlnPro	102
OY		313	GAAGATTTCGAACCTTACTTTGTCAAACGGCTAATAAGTTTCCGTAACTTTTGTTGAG	372
Dd		103	GluAspPheAlaThrTyIryTyCysGlnGlnIryTyLysSerTyProIrrPhrPheGlyGln	122
OY		373	GGAACCAAGCTGGAGATCAAA	393
Dd		123	GlyThrIryValGlnIleIrys	129

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RESULT 5
US-08-812-586-45
: Sequence 45, Application US/08812586
: Patent No. 6048704
:
: GENERAL INFORMATION:
: APPLICANT: Martin David Tilson
: TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
: TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 61
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/812,586
: FILING DATE: 07-MAR-1997
:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 0575/53862-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
:
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 233 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-812-586-45
:
: Alignment Scores:
: Prid. No.: 2,53e-52 Length: 233
: Score: 550.00 Matches: 106

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Percent Similarity:	97.374	Conservative:	5
Best Local Similarity:	92.988	Mismatches:	13
Query Match:	72.274	Indels:	0
DB:	3	Gaps:	0

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		.....	
Db	23	GLINLHTHGLINSEIPROSESERVALSERIALSERVALGLYAPAPVALTHHILETHR	42
Oy	139	TGTCGGGCGAGTCAGGATATTATGCACTGGTATGCTGTATCAGATAAACAGGTAA	198
Db	43	CYARARALASERGLINLYLESESERTRIPHEALATPIYRGINGLINLYPROGLYLYS	62
Oy	199	GCACTTAAGCTCCGTATCTATGCTGCATCCAGTTTGCAAGGTGGTGTCCATCAAGGTTCC	256
Db	63	ALAPROLYSEULENULIETRYSERIALASERLEUGINSERGLYALPROSERARGHE	82
Oy	259	AGCGGAAGTGGATCTGGGACAGATTTCACCTCACCACATCAGCAGCTGACGCTGGAAGAT	318
Db	83	SERGLYSERGLYSERGLYTHIRASPHESERLEUTHIRILESESERLEUGINPROGLIASP	102
Oy	319	TTTGGCAACTACATTTGCAACAGGCTAATGTTCCGCTACACTTTGGTCAGGGAACC	378
Db	103	SERALATHIRYTRYCYSGINGINALASNSERPIEPROLYTRHPHEGLYINGLYTHR	122
Oy	379	AGGTGAGAGATCAAAAGCACTGGGTGCACCATCTGTCTTC	420
Db	123	LYEVALGLINLILEYSAFTHRVALAALAPROSERVALPHE	136

## RESULT 6

; Sequence 26, Application US/08470139

GENERAL INFORMATION:

**TITLE OF INVENTION:** Interleukin-5 specific recombinant antibodies

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO

APPLICATION NUMBER: US/08/470,139

CLASSIFICATION: 536

NAME: TRUJILLO, DOREEN YATKO

REFERENCE/DOCKET NUMBER: CARP-0044

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

TOPOLOGY: linear

US-08-470-139-26

Alignment Scores:

**Score:**

Best Local Similarity

DB:

US-08-728-463B-220 (1-420) X US-08-470-139-26 (1-128)

QY  
13 ATGATGGTCCACGCTCAGCTCTCTCGGTCTTCCTGCCTCGSTTCCCAAGSTTCCAGATGC 72

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: Sequence 1 Application US/08468671
: Patent No. 5648077
: GENERAL INFORMATION:
: APPLICANT: Ostberg, Lars G.
: TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
: TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,671
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/259,372
: FILING DATE: 14-JUN-1994
: APPLICATION NUMBER: US 07/871,426
: FILING DATE: 21-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/676,036
: FILING DATE: 27-MAR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/538,796
: FILING DATE: 15-JUN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/192,754
: FILING DATE: 11-MAY-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/925,196
: FILING DATE: 31-OCT-1986
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 06/904,517
: FILING DATE: 05-SEP-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-50-7
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 128 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-468-671-14

Prid. No.: 1,836-55 length: 128
Score: 578.00 Matches: 110
Percent Similarity: 94.35% Conservative: 7
Best Local Similarity: 88.71% Mismatches: 7
Query Match: 75.95% Indels: 0
DB: 1 Gaps: 0

US-08-728-463B-220 (1-420) x US-08-468-671-14 (1-128)

QY 25 GCTCAGCTCTCGGTCTCTGCTGTGTTCCAGTTCCAGATGCAGATCCAGATG 84
Db 5 AAGlennuenglyleuenuleuenuleutprhnefiroglSerArgCyaspilleglnmet 24
85 ACCCAGTCTTCATCTTCGTTGCTGTGCATCTGTNGAGACAGATCAACATCATCTTGTCCG 144

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Db 25 ThrGlnSerProSerSerValSerAlaSerValGlyAlaPheValThrValThrCysArg 44  
145 GCGAGTCAGGATATTAGCAGCTGGTTAGCTGGTATCAGATAAACGAGTAAAGCACT 204  
Db 45 AlAserdGnGlyLeSerSerTrpPheuAlatPrpYrGnGlnGlnLysProGlyLysAlaPro 64  
Qy 205 AAGCTCTGATTCANAGCTGCATCCAGATTCGCAAAAGTGATGCCATCAAGGTTACGCGGA 266  
Db 65 LysLeuLeuLeuLeuAlaAlaSerSerLeuGlnSerGlyValProSerArgPheIleGly 84  
Qy 265 AGGAGACTGGGACACATATTCACCTCCACATACAGACGCTCGAGCCGGAAGATTTCGA 324  
Db 85 SerGlySerGlyThrAspPheThrIleuThrIleuTrsSerLeuGlnAlaGluAspPheAla 104  
Qy 325 ACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAACCAAGCTG 384  
Db 105 ThrTyrTyrCysGlnGlnAlaAspSerLeuProPheTrpPheGlyGlyGlyThrLysVal 124  
Qy 385 GAGATCAACGA 396  
Db 125 AspPheLysArg 128

```

RESULT 4
US-08-217-918-2
Sequence 2, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Cre
STREET: 379 Lyon Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-918-2

Alignment Scores:
Pred. No.: 1.04e-53
Score: 562.00
Percent Similarity: 92.13%
Best Local Similarity: 82.68%
Query Match: 73.85%
1
DB: 0
US-08-728-463B-220 (1-420) x US-08-217-918-2 (1-129)

```





Db 1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuThrAspAlaArgCys 20  
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGTCATCTGTAGAGACAGATCACC 132  
Db 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40  
QY 133 ATCACTTGTTGGGGGATTCAGATATTAGCAGCTGGTTAGCTGTATTCAGCATTAACA 192  
Db 41 IleThrCysLeuAlaSerGlnGlyIleSerSerTyLeuAlaTrpTyrgInGlnLysPro 60  
QY 193 GGTAAAGCACCTAAGTCTCGATCTATGCTATGCTAGCTAGTTGCAAGTGGTCCCATCA 252  
Db 61 GlyValAlaProIysLeuLeuIleTyrgIlyAlaAsnSerLeuGlnIntrGlyValProSer 80  
QY 253 AGCTTCAGCGAAGTGGATCTGGAGCATTTTCACTCTCACCATCAGCAGCTTCAGCCT 312  
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyThrLeuThrIleSerSerLeuGlnPro 100  
QY 313 GAAGATTTTGCACTTACTATTGTGCAACAGGCTAATAGTTCCCGTACACTTTGGTCAG 372  
Db 101 GluAspPheAlaThrTyTyTyCysGlnGlnSerTyIysPheProAsnThrPheGlyGln 120  
QY 373 GGAACCAAGCTGGAGATCAACAGA 396  
Db 121 GlyThrIysValGlnValLysArg 128

## RESULT 7

US-09-347-061-26  
Sequence 26, Application US/09347061  
Patent No. 6316227  
GENERAL INFORMATION:  
APPLICANT: Bodmer, Mark  
APPLICANT: Achwal, Diljeet Singh  
APPLICANT: Emtage, John Spencer  
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies  
FILE REFERENCE: CARP-0071  
CURRENT APPLICATION NUMBER: US/09/347, 061  
CURRENT FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 26  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: No. 6316227el Sequence  
US-09-347-061-26

## Alignment Scores:

Pred. No.: 3,55e-52 Length: 128  
Score: 548.00 Matches: 104  
Percent Similarity: 89.84% Conservative: 11  
Best Local Similarity: 81.25% Mismatches: 13  
Query Match: 72.01% Indels: 0  
DB: 4 Gaps: 0

US-08-728-463b-220 (1-420) x US-09-347-061-26 (1-128)

QY 13 ATGATGTCCTCCAGCTCAGCTCCTCGGTCTCTGCTGCTGTTCCAGGTTCCAGATGC 72  
Db 1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuThrAspAlaArgCys 20  
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGTCATCTGTAGAGACAGATCACC 132  
Db 21 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr 40  
QY 133 ATCACTTGTTGGGGGATTCAGATATTAGCAGCTGGTTAGCTGTATTCAGCATTAACA 192  
Db 41 IleThrCysLeuAlaSerGlnGlyIleSerSerTyLeuAlaTrpTyrgInGlnLysPro 60  
QY 193 GGTAAAGCACCTAAGTCTCGATCTATGCTATGCTAGCTAGTTGCAAGTGGTCCCATCA 252

Db 61 GlyValAlaProIysLeuLeuIleTyrgIlyAlaAsnSerLeuGlnIntrGlyValProSer 80  
QY 253 AGCTTCAGCGAAGTGGATCTGGAGCATTTTCACTCTCACCATCAGCAGCTTCAGCCT 312  
Db 81 ArgPheSerGlySerGlySerAlaThrAspTyThrLeuThrIleSerSerLeuGlnPro 100  
QY 313 GAAGATTTTGCACTTACTATTGTGCAACAGGCTAATAGTTCCCGTACACTTTGGTCAG 372  
Db 101 GluAspPheAlaThrTyTyTyCysGlnGlnSerTyIysPheProAsnThrPheGlyGln 120  
QY 373 GGAACCAAGCTGGAGATCAACAGA 396  
Db 121 GlyThrIysValGlnValLysArg 128

## RESULT 8

US-08-812-586-16  
Sequence 16, Application US/08812586  
Patent No. 6048704  
GENERAL INFORMATION:  
APPLICANT: Martin David Tilson  
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC  
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)  
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,586  
FILING DATE: 07-MAR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/53862-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-812-586-16

## Alignment Scores:

Pred. No.: 2,46e-51 Length: 235  
Score: 541.00 Matches: 105  
Percent Similarity: 86.03% Conservative: 12  
Best Local Similarity: 77.21% Mismatches: 19  
Query Match: 71.09% Indels: 0  
DB: 3 Gaps: 0

US-08-728-463b-220 (1-420) x US-08-812-586-16 (1-235)

QY 13 ATGATGTCCTCCAGCTCAGCTCCTCGGTCTCTGCTGCTGTTCCAGGTTCCAGATGC 72  
Db 3 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuThrProGlyAlaArgCys 22  
QY 73 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGTCATCTGTAGAGACAGATCACC 132  
Db 23 AlaIleArgIleAlaGlnSerProSerSerLeuSerAlaSerThrGlyAspArgValThr 42

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/164,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-553-48

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Alignment Scores:	
Prod. No.:	5.38e-50
Score:	117
Percent Similarity:	528.00
Best Local Similarity:	93.04%
Best Local Similarity:	90.43%
Query Match:	69.38%
DB:	4
	Gaps: 0

Oy	1	ATGATGGTCCACCACTAGCTCCCTGGGTCTTCGAGCATCTGGGTCCAGATTCCAGATG	72
Oy	13	ATGATGGTCCACCACTAGCTCCCTGGGTCTTCGAGCATCTGGGTCCAGATTCCAGATG	72
Db	3	MetArgValIleuAlaGlnIleuLeuGlyIleuLeuLeuLeuCysPheProGlyAlaArgCys	22
Oy	73	GACATCCAGATGACCCAGTCTCCATCTTCGGTCTGCATCTGTAAGGAGACAGTCAAC	132
Db	23	AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgValThr	42
Oy	133	ATCATCTGTGGGGCGAGTACAGGATATTACAGGTGGTATGACCTGGTATACACATTAACA	192
Db	43	IleMetCysArgAlaSerGlnGlyIleSerSerTyrPheAlaIleTyrGlnGlnIlePhePro	62
Oy	193	GGTAAAGCACCTTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGTGCTCCATCA	252
Db	63	GluIysAlaProIysSerIleuIleTyrAlaAlaSerSerLeuGlnIleSerGlyValProSer	82
Oy	253	AGTTTCAGCGAAGATGATCTGGGACAGATTTCACCTCAGCATCAGACGCTCGAGCCT	312
Db	83	ArgPheSerGlySerGlySerGlyIleThrAspMetIleuLeuIleIleSerSerLeuGlnPro	102
Oy	313	GAAGATTTTGCACTTAATTGATCAACAGGCTAAATATGTTCCCG	357

Db 103 Gluspspeall  
RESULT 11  
US-08-758-417A-313  
Sequence 313, Application US/  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
                    Kay, Robert M.  
TITLE OF INVENTION: Transgenic  
                    Producing He-300129-Human Animals for  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend  
STREET: Two Embarcadero Center, El  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIA TYPE: floppy disk

? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent Release #1.0, Version #1.3G  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/758,412A  
 ? FILING DATE: 02-Dec-1996  
 ? CLASSIFICATION: <Unknown>  
 ? PRIOR APPLICATION DATA: US 08/736,463

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ATTORNEY/AGENT INFORMATION:  
NAME: Seratfin, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 313:  
SEQUENCE CHARACTERISTICS:

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?      LENGTH: 117 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      SEQUENCE DESCRIPTION: SEQ ID NO: 313
US-08-758-417A-313

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Alignment Scores:		
Pred. No.:	5.38e-50	117
Score:	528.00	Matches: 1040
Percent Similarity:	93.04%	Conservative: 3
Best Local Similarity:	90.43%	Mismatches: 8
Query Match:	69.38%	Indels: 0
DB:	4	Gaps: 0

US-08-728-463B-220 (1-420) X US-08-758-417A-313 (1-117)

QY	121	TGGCGTGTCAATGGTGGGTCCTTCATGGTGTACTACTGAGGTGATCCGCGACGCCCA	180
QY	41	CysAlaValTyrGlySerPheSerGlyTyrTyrTTPSerTTPLeuGlnProPro	60
QY	181	GGTAAAGGGCTGGAGTGATTTGGGGAATCAATCATATGGAGACCACTAACACCCG	240
Db	61	GlyLeuGlyPheGluTrrPileGlyGluIleAsnHisSerGlySerThrAsnTyrAsnPro	80
QY	241	TCCCTCAAGGTGAGACCATATAGTCGACAGTCCAGAACCACTTCCCTGAG	300
Db	81	SerLeuIleSerTyrValThrIleSerValAspIleMetLeuValAsnGlnPheSerLeuLys	100
QY	301	CTGAGCTCTGTGACCCGCCGCGACACGGCTGTGTATTACTGTGCGAGA-----	348
Db	101	LeuSerSerValThrIleAlaAspTrnAlaValTyrTyrCysAlaIleGlyIlePheAla	120
QY	349	-----GTAAATTATGGTTTGGACCCCTGGGGGCGAGGAAACCTGTACACGTCCTCCA	402
Db	121	AlaThrIleValGlnSerPheSerTyrTTPGlyGlnGlyThrLeuValThrValSerSer	140

## RESULT 2

Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)  
C|Species: Homo sapiens (man)  
C|Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C|Accession: S78052; S23717  
R|Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A|Reference number: S78051  
A|Accession: S78052  
A|Molecule type: mRNA  
A|Residues: 1-140 <HAW>  
A|Cross-references: EMBL:X54441, NID:G37815; PIDN:CAA8308.1; PID:G930118  
R|Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burrastero, S.E.; Wilder, R.L.; Nockings  
Int. Immunol. 3, 865-875, 1991  
A|Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A|Reference number: S23716; MUID:92031262; PMID:1718404  
A|Accession: S23717  
A|Molecule type: mRNA  
A|Residues: 15-111 <HAW>  
A|Cross-references: EMBL:X54441  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: immunoglobulin  
F.1-14/Domain: signal sequence (fragment) #status predicted <Sig>  
F.15-140/Product: Ig heavy chain (fragment) #status predicted <Mat>  
F.129-111/Domain: immunoglobulin homology <Imm>

**Alignment Scores:**

Pred. No.:	1.55e-49	Length:	140
Score:	639.50	Matches:	129
Percent Similarity:	90.00%	Conservative:	2
Best Local Similarity:	88.57%	Mismatches:	11
Query Match:	86.07%	Indels:	3
DB:	2	Gaps:	2

US-08-728-463B-205 (1-403) X S78052 (1-140)

QY	16	TTCTTCTCCTCCGAGTGGAGAGCTCCCAAGTGGGTCTGTCCCAAGTGAAGTCAAGAG	75
Db	1	PhePheLeuLeuLeuValAlaAlaProArgTyrValLeuAlaGlnValGlnLeuGln	20
QY	76	TGGGGCGCAGAGACTGTGGAAGCCTTGTGGAGACCTGTCCCTCACTGCGCTGTATAGT	135
Db	21	TrpGlyAlaGlyLeuLeuLeuLysProSerGlnThrLeuSerLeuThrCysAlaValAlaTyrGly	40
QY	136	GGGTCTTTCAGTGGTTACTACTGAGCTGGATATCCGCAAGCCCCAGAGTAAGGGCTGGAG	195
Db	41	GlySerPheSerArgTyrTyrTyrPheSerTyrPheArgGlnProGlyLysGlyLeuGln	60
QY	196	TGAGTTGGGGAAATCATCATATAGGAGAGACCAATACAAACCGCTCCCTCAAGGTGGA	255
Db	61	TrpIleGlyGlnIleAsnHisSerGlySerThrAsnTyrAsnProSerLeuLysSerArg	80

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QY      316 GCCCGGACAGCGGTGTATTACTGTGCG-----AGAGTATTAAAT 357
Db      101 AAlAlAspThrAlaValTyrTyrGysAlaArgGlyGlySerValLeuArgPheLeuGlu 120
QY      358 TGG-----TTGACCCCTGGGGCCAGGAAACCTGATCAACCGTCTCTCA 402
Db      121 TrpLeuLeuTyrProlaIleAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 140

```

RESULT 3  
137782

Ig variable region (VDJ) (clone T23-9) - human (fragment)  
C.Species: Homo sapiens (man)  
C.Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C.Accession: J37782, S25476  
R.Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A.Title: Somatic diversification in the heavy chain variable region genes expressed by  
A.Reference number: A36876; MUID:94119917; PMID:8290556  
A.Accession: J37782  
A.Status: Preliminary  
A.Molecule type: mRNA  
A.Residues: 1-140 <RES>  
A.Cross-references: EMBL:X67906; NID:g33582; PIDD:CAA48104.1; PID:g33583  
C.Superfamily: Immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IIM>

**Alignment Scores:**

Pred. No.:	2.93e-46	Length:	140
Score:	603.00	Matches:	119
Percent Similarity:	87.86%	Conservative:	4
Best Local Similarity:	85.00%	Mismatches:	11
Query Match:	81.16%	Indels:	6
DB:	2	Gaps:	2

US-08-728-463B-205 (1-403) X I37782 (1-140)

QY	ATGAAACACCTGGAGTTCTTCCCTCCCTCGGAGGAGCTCCCAATGGATCTGTCCAG	60
Db	1 MetlyshIleuThrPhePheIleuIleuValAlaAlaProHgtYrValIleuSerGln	20
QY	61 GTGAGCTACAGCAGTGGGGCGCAGAGCTGTGAAGCCTTGAGACCCTCTCCCTCAC	120
Db	21 ValGlnIleuIleuIleuSerGlyProGlyIleuValIysProSerGlnThrIleuSerIleuThr	40
QY	121 TGCCTCTCTATAGTGGGATCTTCACAGTGATTCCTAGACTGGATCCGCACACCCCA	180
Db	41 CysThrValSerGlyIleuSerIleuSerGlyrYrTrpSerTrpIleuArgIleuProPro	60
QY	181 GGTAAAGGGGCTGGAGTGGATTTGGGAAATCAATCACTAGTGAAGCACTATACACCG	240
Db	61 GlyIleuSerIleuIleuTrpIleuGlyrYrIleuYrTrpSerGlySerThrAsnTrpAsnPro	80
QY	241 TCCCTCAAGAGTGAAGTACACCATATCAGTCGACAGCTCCAAAGACCAAGTCTCCCTGAG	300
Db	81 SerIleuSerSerArgIleuThrIleuSerValAspThrSerIysAsnGlnPheSerIleuIys	100
QY	301 CTGAGCTCTGTGACCCGCCGCGACACAGCGTGTATTACTGTGGGAGA-----GTATT	355
Db	101 LeuSerSerValThrAlaAlaSerThrAlaValIYrYrCysAlaArgHisAsnSerSer	120
QY	355 AATTTG-----TTGACCCCTTGGGGCCAGGAGAACCTGTGGTCCAGCTCTCTCA	402
Db	121 SerTrpTrpGlyArgTrpPheAspGlyrTrpGlyGlnGlyThrIleuValThrValSerSer	140

RESULT 4

S47010

ig heavy chain V4.21-Uniqueid-j5 region - human

CISpecies: Homo sapiens (man)

## RESULT 4

Ig heavy chain V4.21-UniqueD-J5 region - human  
C;Species: Homo sapiens (man)

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 3, 2003, 08:56:26 ; Search time 17.0465 Seconds  
(without alignments)  
4545.477 Million cell updates/sec

Title: US-08-728-463B-205  
Perfect score: 743  
Sequence: 1 ATGAACACCTGTTCTT.....CTGTGACCGTCTCTCAG 403

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_n2p.model -DEV=xlp  
-Q=/cgr21/USFTO.spool/US08728463.r/unat\_03062003\_085615\_16827/app\_query.fasta\_1.3690  
-DB=PIR-73 -QMT=faetan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=us08728463@cgrn 1.1.177 @unat\_03062003\_085615\_16827 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR-73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	679	91.4	140	A49045	Ig heavy chain V r
2	639.5	86.1	140	S78052	Ig heavy chain pre
3	603	81.2	140	I37782	Ig variable region
4	593.5	79.9	126	S47010	Ig heavy chain V4.
5	590	79.4	147	S13519	Ig heavy chain V r
6	581.5	78.3	137	S31676	Ig heavy chain V r
7	579	77.9	139	S31586	Ig heavy chain V r
8	578	77.8	146	G1H0H2	Ig heavy chain pre
9	577	77.7	155	S31511	Ig heavy chain - h
10	576	77.5	133	PS0341	Ig heavy chain V-D
11	573	77.1	155	S31512	Ig heavy chain - h
12	569.5	76.6	139	S31686	Ig heavy chain V r
13	569.5	76.6	145	S78055	Ig heavy chain pre
14	554	74.6	146	S09711	Ig heavy chain V r

15	550	74.0	116	2	B26340	Ig heavy chain pre
16	550	74.0	143	2	B49028	Ig heavy chain V-I
17	542	72.9	140	2	A24770	hypothetical hybrid
18	541	72.8	146	2	S09710	Ig heavy chain V r
19	539	72.5	118	2	A26340	Ig heavy chain pre
20	538	72.4	116	2	S18557	Ig heavy chain V r
21	536.5	72.2	231	2	B23746	Ig Fab region IV-J
22	530	71.3	122	2	JI0047	Ig heavy chain V r
23	525.5	70.7	130	2	S31673	Ig heavy chain V r
24	525	70.7	130	2	S31690	Ig heavy chain V r
25	519	69.9	124	2	S31684	Ig heavy chain V r
26	518	69.7	97	2	S26898	Ig heavy chain V r
27	516.5	69.5	137	2	S31585	Ig heavy chain V r
28	516	69.4	135	2	S78051	Ig heavy chain pre
29	512.5	69.0	139	2	A41287	Ig heavy chain pre
30	510.5	68.7	143	2	B41287	Ig heavy chain pre
31	509	68.5	97	2	S14474	Ig heavy chain V r
32	508	68.4	97	2	G34964	Ig heavy chain V-I
33	500	67.3	114	2	I72667	cold agglutinin FS
34	497.5	67.0	117	2	E34964	Ig heavy chain pre
35	490	65.9	97	2	S26805	Ig heavy chain V r
36	485	65.9	123	2	S30530	Ig heavy chain V r
37	485	65.3	135	2	S31604	Ig heavy chain V r
38	483	65.0	97	2	S26806	Ig heavy chain V r
39	483	65.0	97	2	JH0428	Ig gamma chain V r
40	475	63.9	123	2	S30529	Ig heavy chain V r
41	472	63.5	97	2	S26808	Ig heavy chain V r
42	470.5	63.3	120	2	PT0370	Ig mu chain precur
43	466.5	62.8	130	2	S30534	Ig heavy chain V r
44	465	62.6	109	2	PH1673	Ig heavy chain V r
45	464.5	62.5	129	2	S44114	Ig heavy chain V r

## ALIGNMENTS

RESULT 1  
A49045  
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
R/Gilliot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassegni, L.Z.; Labaune, S.; Silverm  
Eur. J. Immunol. 22, 1781-1788, 1992  
A/Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i b  
A/Reference number: A49045, PMID:92324290, PMID:1623923  
A/Accession: A49045  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-140 <GRI>  
A/Cross-references: GB:S39381, NID:G250899, PIDN:AAB22441.1, PID:G250900  
A/Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P.108089)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-116/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	4,39e-53	Length:	140
Score:	679.00	Matches:	129
Percent Similarity:	93.57%	Conservative:	2
Best Local Similarity:	92.14%	Mismatches:	3
Query Match:	91.39%	Indels:	6
DB:	2	Gaps:	1

US-08-728-463B-205 (1-403) x A49045 (1-140)

QY	1	ATGAACACCTGTTCTTCTCTCTGTCGACGCTCCAGATGGCTGCTCCAG	60
DB	1	MeLLYHHIeLeuTrpHePheLeuLeuValAlaAlaProArgrTrpValIleuSerGln	20
QY	61	GTCGACCTACAGACAGTGGCGGAGACGACCTTGAACCTTCGAGACCCGCTCCAC	120
DB	21	ValGlnLeuGlnInTrpGlyAlaGlyLeuLeuLysProSerGlnTrpLeuSerLeuThr	40

QY 121 TGGCTGTCTATGATGGGTCCTTCAAGTGTACTGAGCTGATCCGACGCCCA 180  
DB 41 CysThrValSerGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla 60  
QY 181 GGTAAAGGGCTGAGATGGATTTGGGAATCAATCATATGTGGAAGCACCAATCAACCCG 240  
DB 61 GlySerGlyLeuGlnTrpIleGlyArgIleTyrThrSerGlySerThrAsnPro 80  
QY 241 TCCTCAAGAGTGGAGTACCATATGATGACACCGCCCAAGAACCACTCTCCCTGAAG 300  
DB 81 SerLeuSerSerArgValThrMetSerValAspThrSerGlySerGlnPheSerLeu 100  
QY 301 CTGAGCTCTGTGACCCCGCGGACACAGCGCTGTGATTACTGTGCGAGA-----GTA 351  
DB 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrValAlaArgAspAlaProLeu 120  
QY 352 ATTAATTGTTTCACCCCTGGGCGCAGGAAACCTGTCAACCTCTCTCTCA 402  
DB 121 MetTyrGlyMetAspValTyrGlyGlnGlyThrThrValThrValSerSer 137

## RESULT 7

S31586  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31586  
R/Cuiquier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31586  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-139 <CUI>  
A/Cross-references: EMBL:Z14196; NID:G30978; PIDN:CAH78565.1; PID:G30979  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/3-4-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2.5e-44 Length: 139  
Score: 581.50 Matches: 115  
Percent Similarity: 85.61% Conservative: 4  
Best Local Similarity: 82.73% Mismatches: 15  
Query Match: 78.26% Indels: 5  
DB: 2 Gaps: 1

US-08-728-463b-205 (1-403) x S31586 (1-139)

QY 1 ATGAACACCTGATGGTCTTCTCTCTCTGAGCTCCAGATGGGTCCTGCCAG 60  
DB 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProAlaGlyValLeuSerGln 20  
QY 61 GTGACGATACAGCAGTGGGCGCAGAGCTGTGAAGCTTCGAGACCTGTCCCTGACC 120  
DB 21 ValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGlnTrpLeuSerLeuThr 40  
QY 121 TGGCTGTCTATGATGGGTCCTTCAAGTGTACTGAGCTGATCCGACGCCCA 180  
DB 41 CysThrValSerGlySerIleSerSerTyrTyrTrpSerTrpIleArgGlnProAla 60  
QY 181 GGTAAAGGGCTGAGTGGATTTGGGAATCAATCATATGTGGAAGCACCAATCAACCCG 240  
DB 61 GlySerGlyLeuGlnTrpIleGlyArgIleTyrThrSerGlySerThrAsnPro 80  
QY 241 TCCTCAAGAGTGGAGTACCATATGATGACACCGCCCAAGAACCACTCTCCCTGAAG 300  
DB 81 SerLeuSerSerArgValThrMetSerValAspThrSerGlySerGlnPheSerLeu 100  
QY 301 CTGAGCTCTGTGACCCCGCGGACACAGCGCTGTGATTACTGTGCGAGA----- 348  
DB 101 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyGlyLeuGly 120

QY 349 ---GTAATTATGTTTCACCCCTGGGCGCAGGAAACCTGTGATCCCTCTCTCA 402  
DB 121 IleArgArgGlyAlaAlaPheAspIleTrpGlyGlnGlyThrMetValThrValSerSer 139

## RESULT 8

IGHH2  
Ig heavy chain precursor V-II region (ARR-77) - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 02-Sep-1997  
C/Accession: A02101  
R/Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.  
Gene 33, 181-189, 1985  
A/Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequ  
A/Reference number: A02101; MUID:85205332; PMID:3922855  
A/Accession: A02101

A/Molecule type: mRNA  
A/Residues: 1-146 <KUD>  
A/Note: the sequence was determined from the differentiated gene  
A/Note: the authors translated the codon GGG for residue 17 as Arg  
C/Genetics:  
A/Gene: GDB:IGHV@  
A/Cross-references: GDB:128528; OMIM:147070  
A/Map position: 14q32.33-14q32.33  
A/Intons: 16/3  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-146/Product: Ig heavy chain V-II region (ARR-77) #status predicted <MAT>  
F/3-117/Region: V segment  
F/35-117/Domain: immunoglobulin homology <IMM>  
F/118-127/Region: D segment  
F/128-146/Region: J segment  
F/42-115/Dissulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 4.2e-44 Length: 146  
Score: 579.00 Matches: 118  
Percent Similarity: 83.67% Conservative: 5  
Best Local Similarity: 80.27% Mismatches: 11  
Query Match: 77.93% Indels: 14  
DB: 1 Gaps: 3

US-08-728-463b-205 (1-403) x G1HH2 (1-146)

QY 1 ATGAACACCTGATGGTCTTCTCTCTCTGAGCTCCAGATGGGTCCTGCCAGTGG 56  
DB 1 MetLysHisLeuTrpPhePheLeuLeu-TyrCysGlnLeuProAspValGlyValLeuSe 20  
QY 57 CCAAGTACAGCTACAGCAGTGGGCGCAGAGCTGTGAAGCTTCGAGACCTGTCCCT 116  
DB 20 GlnValGlnLeuGlnGlnTrpIleGlyValGlyLeuValLysProSerGlnThrLeuSerIle 40  
QY 117 CACCTGCTGTATGATGGGTCCTTCAAGTGTACTGAGCTGATCCGACGCCA 176  
DB 40 ValThrCysAlaValAlaPheGlyGlySerPheSerGlyTyrTyrTrpSerTrpIleArgGlnPr 60  
QY 177 CCAAGTAAAGGGCTGAGTGGATTTGGGAATCAATCATATGTGGAAGCACCAATCAAC 236  
DB 60 OProGlyArgGlyLeuGlnTrpIleGlyGlnIleAsnHisSerGlySerThrAsnTyrLys 80  
QY 237 CCGCTCCCTCAAGAGTGCAGTACCATATGATGACGACGTCGACCAAGACCAAGTTCTCCCT 296  
DB 80 ThrSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnLeuPheSerIle 100  
QY 297 GAAGTGAAGCTCTGTGAACCGCGGACACAGCGCTGTGATTACTGTGCGAGATAAT-- 354  
DB 100 WlySerLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyLeuSe 120  
QY 355 -----AATTGG-----TTGACACCCCTGGGCGCAGGGAAC 383  
DB 120 WArgGlyGlyTyrPAsnAspValAspTyrTyrTyrGlyMetAspValTyrPoiGlnGly 140

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C/Accession: S47010  
 R:Mahmoud, M.; Gasyra, E.; Denonne, G.; Edwards, J.; Bell, D.; Cairns, E.  
 submitted to the EMBL Data Library, July 1994  
 A/Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bfr  
 A/Reference number: S47009

A/Accession: S47010  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-126 <NMH>  
 C/Cross-references: EMBL:Z35492; NID:9517254; PIDN:CAA84625.1; PID:9517255  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-97/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	2,09e-45	Length:	126
Score:	593.50	Matches:	113
Percent Similarity:	89.68%	Conservative:	0
Best Local Similarity:	89.68%	Mismatches:	2
Query Match:	79.88%	Indels:	11
DB:	2	Gaps:	1

US-08-728-463b-205 (1-403) x S47010 (1-126)

```

QY 58 CAGGTGACGTACAGCAGTGGGCGCAGACGTGTGAGCCTTCGAGACCTGCTCCCTC 117
Db 1 GlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLeuProSerGluThrLeuSerLeu 20
QY 118 ACTGGGCTGTCTAAGTGGGCTCTTCACTGCTTACTGAGAGCTGGATCCGCGACCC 177
Db 21 ThCysAlaValValTrpGlySerPheSerGlyTrpTrpSerTrpPheArgGlnPro 40
QY 178 CCAGTAAGGGGCTGAGTGGATTGGGGAATCATCATAGTGAAGACCAACTACAC 237
Db 41 ProGlyLysGlyLeuGlnTrpIleGlyGlnIleSerHisSerGlySerThrAsnTrpAsn 60
QY 238 CCGTCCCTCAAGAGTCAGTCAACATATCAGTCGACACGTCAAGAACAGTTCTCCCTG 297
Db 61 ProSerLeuLeuSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeu 80
QY 298 AACCTGAGCTCTGACCCCGCGGACACCGCTGTATTACTGTGCGAGA----- 348
Db 81 LysLeuSerSerValThrAlaAlaSerThrAlaValTrpTrpCysAlaArgGlyGlyGln 100
QY 349 -----GTAATTAATTGGTTCGACCCCGGCGGCGCAGGAGCC 384
Db 101 CysProLysLysAlaSerCysTrpTrpLysAsnTrpPheAspProTrpGlyGlnGlyThr 120
QY 385 CTGGTCAACCGCTCTCTCA 402
Db 121 LeuValThrValSerSer 126

```

## RESULT 5

ig heavy chain V region precursor - human

C/Species: Homo sapiens (man)  
 C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S13519  
 R:Morcari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
 Nucleic Acids Res. 19, 673, 1991  
 A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
 A/Reference number: S13519; MUID:91187691; PMID:2011556  
 A/Accession: S13519  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-147 <MOR>  
 A/Cross-references: EMBL:X56158; NID:937724; PIDN:CAA39626.1; PID:937725  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/41-125/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	4.32e-45	Length:	147
Score:	590.00	Matches:	116
Percent Similarity:	86.43%	Conservative:	5
Best Local Similarity:	82.86%	Mismatches:	13
Query Match:	79.41%	Indels:	6
DB:	2	Gaps:	2

US-08-728-463b-205 (1-403) x S13519 (1-147)

```

QY 1 ATGAACACCTGTGTTCTTCTCTCCCTCGTGGAGCTCCAGATGGGCTGTCCAG 60
Db 8 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 27
QY 61 GTGCAGCTACAGAGTGGGCGCAGAGCTGTGAACCTTCGAGACCTGTCTCCAC 120
Db 28 LeuGlnLeuGlnLeuSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 47
QY 121 TGGCTGTCTAAGTGGGCTCTTC-----AGTGTACTACTGAGCTGATCCGCGAG 174
Db 48 CysThrValSerGlyGlySerLysSerSerSerTrpTrpGlyTrpGlyTrpIleArgGln 67
QY 175 CCCCCGTAAGGGGCTGAGTGGATTGGGGAATCATCATAGTGAAGACCAACTAC 234
Db 68 ProProGlyLysGlyLeuGlnTrpIleGlySerLysTrpTrpSerLysSerThrTrpTrp 87
QY 235 AACCCGTCCTCAAGAGTCAGTCAACATATCAGTCGACACGTCAAGAACAGTTCTCC 294
Db 88 AsnProSerLeuLeuSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 107
QY 295 CTGAAGCTAGCTCTGTACCCCGCGGACACGGCTGTATTACTGTGCGAGATTAAT 354
Db 108 LeuLysLeuSerSerValThrAlaAlaSerThrAlaValTrpTrpCysAlaArgProLeu 127
QY 355 AATTGG-----TTGACCCCTGGGCGCAGGGAACCTGTGTCACCTCTCTCA 402
Db 128 LeuTrpPheGlyGlnLeuPheAspTrpTrpGlyGlnGlyThrLeuValThrValSerSer 147

```

## RESULT 6

ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31676  
 R:Chisnister, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Reference number: S31585  
 A/Accession: S31676  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-137 <CU1>  
 A/Cross-references: EMBL:Z14182; NID:931031; PIDN:CAA78551.1; PID:931032  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/34-116/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	2.5e-44	Length:	137
Score:	581.50	Matches:	114
Percent Similarity:	86.86%	Conservative:	5
Best Local Similarity:	83.21%	Mismatches:	15
Query Match:	78.26%	Indels:	3
DB:	2	Gaps:	1

US-08-728-463b-205 (1-403) x S31676 (1-137)

```

QY 1 ATGAACACCTGTGTTCTTCTCTCCCTCGTGGAGCTCCAGATGGGCTGTCCAG 60
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20
QY 61 GTGCAGCTACAGAGTGGGCGCAGAGCTGTGAACCTTCGAGACCTGTCTCCAC 120
Db 21 ValGlnLeuGlnLeuSerGlyProGlyLeuValLysProSerGluThrLeuSerLeuThr 40

```



Percent Similarity: 84.51% Conservative: 9  
 Best Local Similarity: 78.17% Mismatches: 14  
 Query Match: 77.52% Indels: 8  
 DB: 2 Gaps: 2

US-08-728-463B-205 (1-403) x S31512 (1-155)

QY 1 ATGAACACCTGGTCTTCTCTCTCTGTCAGACCTCCAGATGGCTCTGTCCAG 60  
 Db 14 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 33  
 QY 61 GTGCAGCTACGACGATGGGGCGACGACTGTGAAGCTTCGAGAACCTGTCTCCAC 120  
 Db 34 ValGlnLeuGlnIleuSerGlyProGlyLeuValIleProSerGlnTrpLeuSerLeuTr 53  
 QY 121 TGGCGCTGTATGATGGTCTCTTCACAGTGTACTACAGACCTGAGACCCGCCCA 180  
 Db 54 CysThrValSerIleGlySerIleSerSerTrpTrpSerTrpIleArgGlnProPro 73  
 QY 181 GTTAAAGGCGCTGAGATGGATTGGGAATCATCATATGATGAAGCACCACTACAC 240  
 Db 74 GlyIleGlyLeuGlnIleTrpIleGlyTrpIleTrpTrpIleSerAlaThrTrpAsnPro 93  
 QY 241 TCCCTCAAGATGAGTACCATATCATGTCAGACGTCACAAACCACTTCTCCAG 300  
 Db 94 ProIleIleSerArgValThrIleSerValAspThrSerIleAsnGlnPheSerLeuLys 113  
 QY 301 CTGAGCTCTGACCCGCGGACAGCGGCTGTATACCTGTCAGAGA-----GTA 351  
 Db 114 ValSerSerValThrAlaAlaPheThrAlaValIleTrpCysAlaArgGlyGlyIle 133  
 QY 352 ATTAATTGTTCT-----GACCCCTGGGGCGGAGAACCTGTCTCACCGTC 396  
 Db 134 SerSerTrpTrpValTrpTrpGlyMetAlaPheValTrpIleGlnIleThrThrVal 153  
 QY 397 TCCCTCA 402  
 Db 154 SerSer 155

## RESULT 12

S31696  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31696  
 R:Chisnier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tommelle, C.  
 Submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31696  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-139 <CDI>  
 A:Cross-references: EMBL:Z14194; NID:930975; PIDN:CA78563.1; PID:930976  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1.45e-43 Length: 139  
 Score: 573.00 Matches: 114  
 Percent Similarity: 83.57% Conservative: 3  
 Best Local Similarity: 81.43% Mismatches: 16  
 Query Match: 77.12% Indels: 7  
 DB: 2 Gaps: 1

US-08-728-463B-205 (1-403) x S31696 (1-139)

QY 1 ATGAACACCTGGTCTTCTCTCTCTGTCAGACCTCCAGATGGCTCTGTCCAG 60  
 Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGln 20  
 QY 61 GTGCAGCTACGACGATGGGGCGACGACTGTGAAGCTTCGAGAACCTGTCTCCAC 120

Db 21 ValGlnLeuGlnIleuSerGlyProGlyLeuValIleProSerGlnTrpLeuSerLeuTr 40  
 QY 121 TGGCGCTGTATGATGGTCTTCTCTCTCTGTCAGACCTCCAGATGGCTCTGTCCAG 180  
 Db 41 CysThrValSerIleGlySerIleSerSerTrpTrpSerTrpIleArgGlnProAla 60  
 QY 181 GTTAAAGGCGCTGAGATGGATTGGGAATCATCATATGATGAAGCACCACTACAC 240  
 Db 61 AlaIleGlyLeuGlnIleTrpIleGlyTrpIleTrpTrpIleSerAlaThrTrpAsnPro 80  
 QY 241 TCCCTCAAGATGAGTACCATATCATGTCAGACGTCACAAACCACTTCTCCAG 300  
 Db 81 SerLeuLysSerArgValThrIleSerSerValAspThrSerIleAsnGlnPheSerLeuLys 100  
 QY 301 CTGAGCTCTGACCCGCGGACAGCGGCTGTATACCTGTCAGAGA-----GTA 348  
 Db 101 LeuSerSerValThrAlaAlaPheThrAlaValIleTrpCysAlaArgGlyLeuGly 120  
 QY 349 -----GTAATTAAATTGTTCTCAACCTGCGGCGGAGAACCTGTCTCACCGTCCT 400  
 Db 121 LeuThrGlyAspIleTrpIleAspTrpTrpGlyGlnIleThrLeu-SerProSerPro 139

## RESULT 13

S78055  
 Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
 C:Accession: S78055; S23720  
 R:Harindranath, N.  
 Submitted to the EMBL Data Library, August 1990  
 A:Reference number: S78051  
 A:Accession: S78055  
 A:Molecule type: mRNA  
 A:Residues: 1-145 <HAR>  
 A:Cross-references: EMBL:X54445; NID:937817; PIDN:CA38312.1; PID:937818  
 R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Bursaturo, S.E.; Wilder, R.L.; Nockin  
 Int. Immunol. 3, 865-875, 1991  
 A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and  
 patient.  
 A:Reference number: S23716; MUID:92031262; PMID:1718404  
 A:Accession: S23720  
 A:Molecule type: mRNA  
 A:Residues: 18-115 <HAM>  
 A:Cross-references: EMBL:X54445  
 A>Note: the authors translated the codon GCA for residue 67 as Arg  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>  
 F:32-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 2.99e-43 Length: 145  
 Score: 569.50 Matches: 114  
 Percent Similarity: 82.07% Conservative: 5  
 Best Local Similarity: 78.62% Mismatches: 13  
 Query Match: 76.65% Indels: 13  
 DB: 2 Gaps: 2

US-08-728-463B-205 (1-403) x S78055 (1-145)

QY 7 CACCTGGTCTTCTCTCTCTCTGTCAGACCTCCAGATGGCTCTGTCCAGTGCAG 66  
 Db 1 HisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeuSerGlnValGln 20  
 QY 67 CTACAGCAGTGGGGCGACGACTGTGAAGCTTCGAGAACCTGTCTCCACCTGCGCT 126  
 Db 21 LeuGlnIleuSerGlyProGlyLeuValIleProSerGlyThrLeuSerLeuTrpCysAla 40  
 QY 127 GTCTAGTGGTGGTCTCTCT--AGTGTACTACTGAGACCTGATCCGACGCCGCCAGCT 183  
 Db 41 ValSerIleGlySerIleSerSerAsnTrpTrpSerTrpValArgGlnProGly 60



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QY 184 AAGGGCTGAGTGGATTTGGGGAATCAATCATATGGAAGACCAACTACACCCGCC 243  
Db 61 LysGlyLeuGlnIurpIleGlyGlnIleTyrlHisSerGlySerThrIleAsnProSer 80  
QY 244 CTCAGAGTCAGTCAACCATATGATGACACCTCCAGAACAGATTCTCTCCGAAAGCTG 303  
Db 81 LeuLysSerAlaValThrIleSerValAspLysSerIleValAsnGlnPheSerLeuLys 100  
QY 304 AGCTCTGTACCGCCCGGACAGCGCTGTATTACTGTGCGAGATTAATAT----- 357  
Db 101 SerSerValThrAlaAspThrAlaValThrTyrlCysAlaIleValThrGlySerThr 120  
QY 358 -----TGCTGACCCCTGGGGCCGAGAACCTG 387  
Db 121 PheTrpSerGlyTyrlTyrlThrArgGlyTyrlTyrlPheAspTyrlTrpGlyGlnGlyThrLeu 140  
QY 388 GTCACCGTCTCTCTCA 402  
Db 141 ValThrValSerSer 145

## RESULT 14

S09711  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S09711  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.  
Biochem. J. 268, 135-140, 1990  
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains C  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/34-118/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	7,38e-42	Length:	146
Score:	554.00	Matches:	110
Percent Similarity:	80.82%	Conservative:	8
Best Local Similarity:	75.34%	Mismatches:	16
Query Match:	74.56%	Indels:	12
DB:	2	Gaps:	2

US-08-728-463B-205 (1-403) x S09711 (1-146)

QY 1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGACGCTCCAGATGGTCTGTCCAG 60  
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaIleProArgTrpCysLeuSerGln 20  
QY 61 GTGACAGTACAGAGTGGGGCGAGACTGTGAAGCTTGGAGACCTGTCTCCAC 120  
Db 21 ValGlnLeuGlnIleSerGlyProGlyLeuValLysProSerGlnThrLeuSerValThr 40  
QY 121 TGGGCTGTATAGTGGGCTCTTC-----AGTGTACTACTAGAGCTGGATCCGCGAG 174  
Db 41 CysThrValSerGlyLysSerValSerSerGlyLeuTyrlTrpSerTrpIleArgGln 60  
QY 175 CCCCCAGTAAAGGGCTGAGTGGATTTGGGAAATCAATCATATGGAAGACCAACTAC 234  
Db 61 ProProGlyLysGlyProGlyIleGlyTyrlIleTyrlSerGlySerThrIleAsnPro 80  
QY 235 AACCCGCTCTCAAGAGTCAAGTCAACCAATCATAGTCAAGCTCCAGAACAGTTCTC 294  
Db 81 AsnProSerLeuArgSerValThrIleSerValAspThrSerLysAsnGlnPheSer 100  
QY 295 CTGAAGCTGAGCTCTGAGACCGCCGAGACAGGCTGTGTATATCTGTGAGAGTAAT 354  
Db 101 LeuLysLeuGlySerValThrAlaIleAspThrAlaValTyrlCysAlaIleValLeu 120

QY 355 -----AATGCTGACCCCTGGGGCCAGGAGACC 384  
Db 121 ValSerArgThrSerIleSerGlnTyrlSerTyrlMetAlaSerValTrpGlyGlyThr 140  
QY 385 CTGTCACCGTCTCTCTCA 402  
Db 141 ThrValThrValSerSer 146

## RESULT 15

B26340  
Ig heavy chain precursor V-II region (71-4) - human  
C/Species: Homo sapiens (man)  
C/Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C/Accession: B26340  
R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986  
A/Title: Organization and evolution of variable region genes of the human immunoglobulin  
A/Reference number: A26340; MUID:87061007; PMID:3097326  
A/Accession: B26340  
A/Molecule type: DNA  
A/Residues: 1-116 <KOD>  
A/Cross-references: GB:X05711; NID:G33602; PIDN:CAA29183.1; PID:9296660  
A/Note: the authors translated the codon GAG for residue 25 as Gln  
C/Genetics:  
A/Intons: 16/1  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/1-19/Domain: signal sequence #status predicted <Sig>  
F/20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
F/34-116/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1.69e-41	Length:	116
Score:	550.00	Matches:	105
Percent Similarity:	93.10%	Conservative:	3
Best Local Similarity:	90.52%	Mismatches:	8
Query Match:	74.02%	Indels:	0
DB:	2	Gaps:	0

US-08-728-463B-205 (1-403) x B26340 (1-116)

QY 1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGACGCTCCAGATGGTCTGTCCAG 60  
Db 1 MetLysHisLeuTrpPhePheLeuLeuValAlaIleProArgTrpValLeuSerGln 20  
QY 61 GTGACAGTACAGAGTGGGGCGAGACTGTGAAGCTTGGAGACCTGTCTCCAC 120  
Db 21 ValGlnLeuGlnIleSerGlyProGlyLeuValLysProSerGlnThrLeuSerValThr 40  
QY 121 TGGGCTGTATAGTGGGCTCTTC-----AGTGTACTACTAGAGCTGGATCCGCGAG 180  
Db 41 CysThrValSerGlyLysSerValSerSerGlyTyrlTrpSerTrpIleArgGlnProPro 60  
QY 181 GGTAAAGGGCTGAGTGGGAAATCAATCATATGGAAGACCAACTACACCCG 240  
Db 61 GlyLysGlyLeuGlnIurpIleGlyTyrlIleTyrlSerGlySerThrIleAsnPro 80  
QY 241 TCCCTCAAGAGTGAAGTCAACATATGATGACGACGCTCCAGAACAGATTCTCTGAG 300  
Db 81 SerLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSerLeuLys 100  
QY 301 CTGAGCTGTGACCCCGCGAGACAGGCTGTGTATATCTGTGCGAG 348  
Db 101 LeuSerSerValThrAlaIleAspThrAlaValTyrlCysAlaIleArg 116

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Job time : 19.0465 secs